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REFERENCE AUTHORS TITLE KEYWORDS SOURCE RESULT 1
HSA295695
LOCUS
DEFINITION
ACCESSION
VERSION REFERENCE TITLE JOURNAL JOURNAL AUTHORS ORGANISM Homo sapiens mRNA for stabilin-2 (STAB2 gene). AJ295695 AJ295695.1 GI:18073427 STAB2 gene; stabilin-2. Politz,O., Gratchev,A., McCourt,P.A.G., Schledzewski,K., Guillot,P., Johannson,S., Birk,R., Hakiy,N., Franke,P., Kodelja,V. Kannicht,C., Orfanos,C.E., Johannson,S. and Goerdt,S. Stabilin-1 and stabilin-2 constitute a novel family of fasciclin domain-containing adhesion molecules associated with endothelial-macrophage differentiation and angiogenic processes Gratchev,A.
Direct Submission
Submitted (27-JUL-2000) Gratchev A., Department of Dermatology, Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Unpublished Homo sapiens (sites) (bases 1 to 8266) Linear PRI 04-JAN-2002 Kodelja, V.,

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LETGRVAYPTAFASQNCGSGVGTUDYGPRPNKSEMMDVFCYEMKDVNCTCKYGYVGD
GFSCSGNLLQVLMSFPSLTUPLTEVLAYSAGGAAFHLTDLSIRGTLFVPQNSG
LGENGTLSGRDIEHHLANVSNFFYNDLVNGTTLQTRLGSKLLLTTASQDPLQPTETRFV
DGRAILQWDIFASNGIIHVISRPLKAPPAPVTLTHTGLGAGIFFAIILVTGAVALAAY
SYFRINGRTIGFQHFESEEDINVAALGKQQPENISNPLYESTTSAPPEPSYDPFTDSE
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CTLINVCLTKNGGCSEFAICHHTGQVERTCTCKPNYIGDGFTCRGSIYQELPKNPKTS
QYFFQLQEHFVKDLVGPGPFTVFAPLSAAFDEEARVKDMDYGLMPQVLHYHVVACHQ
LLLENLKLISNATSLQGEPIVISVSQSTVYINNKAKIISSDIISTNGIVHIIDKLLSP
KNLLITPKDNSGRILQNLTTLATNNGYIKFSNLIQDSGLLSVITDPIHTPVTLFWPTD
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VYWSRCPANSEPTALFTHRCVYSGRFGSLKSGCARYCNATVKLTSKCKGFYGPDCNQC
PGGESNPCSGNGQCADSLGGNGTCICEEGFGGSQCOPCSDPNKYGPRCNKKCLCVYGT
CNNRIDSDGACLTGTCRDGSAGRLCDKQTSACGPYVQFCHIHATCEYSNGTASCICKA
GYEGDGTLCSEMDPCTGITPGGCSRNAECIKTGTGTHTCVCQGGTGNGRDCSEINNC
LAPSAGGCHUNASCLYVGPGQNEDECKKGFRGNGIDCEPTTSCLEQTGKGLPLASCOS
TSSGVWSCVCQEGYEGDGFLCYGNAAVELSFLSEAAIFNRWINNASLQPTLSATSNLT
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EHTFESNNEQTIMTMLQPRYSKFRSLLEETNLGHALDEDGVGGPYTIFVPNNEALNNM
KDGTLDYLLSPEGSRKLLELVRYHIVPFTQLEVATLISTPHIRSMANQLIQFNTTDNG
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GRWGPDCIECPGGAGSPCNGRGSCAEGMEGNGTCSCQEGFGGTACETCADDNLFGPSC
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/db_xref="taxon:9606"
187. .7842
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CQACFGGPDAFCNNRGVCLDQXSATIGECKDFNGTAGEMCWPGRFRFDCLFCGGSD
HGQCDDGITGSGOCLCETGWTGPSCDTQAVLDAVCTPPCSAHAJTCKENNTCECNLDYE
GDGITCTVVDFCKQDNGGCAKVARCSQKGTKVSCSCQKGYKGDGHSCTEIDPCADGLN
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KVLEIQKNRCDNNATTIIRGRCRTCSSELTCPFGTKSLGNEKRRCIYTSYFMGRRTLF
IGCQPKCVRTVITRECCAGFFGPQCQPCPGNAQNVCFGNGICLDGVNGTGVCECGEGF
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GNFLHLAKVDGNITIEGASIVDGDNAATNGVIHIINKVLVPQRRLTGSLPNLLMRLEQ
MPDYPIFRGYIIQYNLANAIEAADAYTVFAPNNNAIENYIREKKVLSLEEDVLRYHVV
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KCGAGRDIGDLFLNGQTCRIYQRELLFDLGVAYGIDCLLIDPTLGGRCDTFTTFDASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGTACETCTEGKYG1HCDQACSCVHGRCNQGPLGDGSCDCDVGWRGVHCDNATTEDNC
NGTCHTSANCLTNSDGTASCKCAAGFQGNGT1CTA1NACE1SNGGCSAKADCKRTTPG
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/protein_id="CAC82105.1"
/db_xref="G1:18073428"
/translation="MMLQHLVIFCLGLVVQNFCSPAETTGQARRCDRKSLLTIRTECR
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187. .
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4730	AGTGTGCACGTGCAAAGCAGGCTACACGGGTGATGGCATTGTGTGCCTGGAAAT	Db
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896 4490	837 ctgtgactgtgacgtcggctggcgaggagtgaagtgtgacatggagatcaccacagacaa	Qy Db
836 4430	777 cgaccaagcatgctcttgtgtccatgggagatgtagccaaggacccttgggagacggctc 	Qy Db
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656 4251	598 tgctg-gctggcttctttggcccacaatgccaagcctgccccgggagaggtcaaaatgtg	Qy Db
597 4191	538 aagagatcogtattcatcgggtgccagccacagtgtgtgagaaccatcattacaagagcc	Оу Дъ
537 4131	481 gagacaaaaccacttagagagacgaggaaatgcatctattccattcattgggg	ОУ
480 4071	421 gacaccattattgtgagagggagtgtggaaagtgttcccagcaagccccctgcccactc	Qy Db
420 4011	361 ggagtgatccatggtctggagaaagttctggaaattcagaagaacagatgtgacaataat 	Qy Db
360 3951	301 aatgaccagctgtatgtaaatgaagctccaataaactacaccaatgtggccactgataaa 	Qy Db
300 3891	241 aacggcatgcaccgagagaccatgctggggttctccttacctccttgccttcttctccgc	Фу
240 3831	181 gaagatattctacggtaccatgtggtcctgggggaaaagctcctgaagaatgacttgcat 	Qy Db
180 3771	121 gtgccaaacaatgaagccatcgaaaactatatcagggagaaggaag	Qy
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2276 5870	tggcattgactgcctactcatgaatcctaccctaggtggccgatgtgacacttttactac	2217 5811
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1916 5510	attcagcaagttgatacaggactcaggcttgctgtcagtca	1857 5451
1856 5450	tgccttgggcagggttctgcaaaatcttactacagtggcagcaaaccacggatataccaa 	1797 5391
1796 5390	cgtcatccacgttatagacaagttgctgtctcccaaaaacttgcttatcacccccaaaga 	1737 5331
1736 5330	cactgtgttcataaacaatgaggcgaaggtcctgtccagtgacatcatcagcaccaatgg	1677 5271
1676 5270	agtgaccacaagtgccacgaccctccaaggagagccagtttccatctctgtctctcagga	1617 5211
1616 5210	gtoccaggttettogetateacgtggtgggetgecagcagetgetgttggacaacetaaa 	1557 5151
1556 5150	tttgtctagctccttcaatcatgagccccggattaaagactgggatcagcagggcctcat	1 497 5091
1496 5090	gttgcaggagcatgctgtccgagagcttgctggacctggccccttcaccgtgttcgcgcc 	1437 5031
1436 5030	ccggggcagcatctacggggagcttcccaagaacccttcgacgtcccagtacttcttcca 	1377 4971
1376 4970	tgagcaagatcaaaggatatgtacctgcaagccagactacacgggtgatggaatcgtctg	1317 4911
1316 4910	tatcaatgtctgcctaacgaacaatggcggctgcagtccatttgccttctgcaactacac	1257 4851
1256 4850	CAACCAGGCTGCCTGTAACTGTTTGCCAGCATACACTGGAGATGGAAAGGTCTGCACACT	1197 4791
4790	CCCGTGTTTGGAGAACCATGGTGGCTGTGACAAGAATGCGGAGTGCACACAGACAG	4731

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6947	ATGCCCAGAAGGCCAAGTACCACCTGTGCTCAGCAGGCTGGCT	6888	Db
3356	tatgcccagaaggccaagtatcacctgtgctcggccggctggct	3297	Qy
6887	CAAAGCCAGAGAGGCCTGTGCCAACGAAGCTGCGACCATGGCAACCTACAACCAGCTCTC	6828	рь
3296	aaagccaaagaagcctgtgccaaagaagctgcgaccatagccacctacaaccagctct		Qy
6827	ACTGT	6768	Dβ
3236	gaccgtaggagtattocatctacgotocccactgggccagtacaaactgacattg	\rightarrow	Qy
6767	CTTACAGGACAATGGGCAGTGCCATGCAGACGCCAAATGTGTCGACCTCCACTTCCAGGA	6708	Db
3176	tacaggacaacggacagtgccaccagatgccagctgtgcagacctctacttccagg	3117	Qy
6707	AAGTCACTATGTCGGAGATGGGCTGAACTGTGAGCCGGAGCAGCTGCCCATTGACCGCTG	6648	Db
3116	agtcactatgtcggggacggagtggactgtgagcctgagcagctgccgctcgaccgtt	3057	Qy
6647	GTGTCACGAGCACGCCACCTGTAAGATGACAGGCCCGGGCAAGCACAAGTGTGAGTGTAA	6588	Db
3056	gccatgagcacgccacctgcaggatgacgggcccaggcaagcataagtgtgaatgta	2997	ОУ
6587	CAAAGGGGACGGGCACAGCTGCACAGAGATAGACCCCTGTGCAGACGGCCTTAACGGAGG	6528	DЬ
2996	aagggggatggctacagctgcatagagatagacccctgtgcagacggtgtcaacgggg	2937	Qy
6527	AAAGGTGGCCAGAATGCTCCCAGAAGGGCACGAAGGTCTCCTGCAGCTGCCAGAAGGGGATA	6468	Db
2936	aaygtcqctaagtgctcccagaaaggcacccaagtctcttgcagctgcaagaaaggct		Qy
6467	AGGTGACGGAATCACATGCACACTTGTGGATTTCTGCAAACAGGACAACGGGGGGTGTGC	6408	Db
2876	ggtgacgggatcacatgcacagtcgtggacttctgcaaacagaaccagaacgagggctgtg	2817	Qy
6407	TIGTTCTGCTCATGCCACCTGTAAGGAGAACAACACGTGTGAGTGTAACCTGGATTATGA	6348	Db
2816	tgctccgtgcacgccacctgtacggagaacaacacgtgtgtgt	2757	Qy
6347	GGGGTGGACAGGCCCCTCGTGTGACACTCAGGCAGTTTTGCCTGCAGTGTGTACGCCTCC	6288	Db
2756	ggtggacagccgcttcgtgtgacactcccacagctgtattcgcagtgtgcacacctg	2697	Qy
6287	CTCAGACCACGGACAGTGCGATGATGGCATCACGGGCTCCGGGCAGTGCCTCTGTGAAAC	6228	Db
2696	tocgagoatggacagtgtgatgaggggatcacaggotccgggggagtgcctctgtgaaa	2637	Qy
6227	GTGGCT	6168	Db
2636	acagcctgcgagctctgctggcatgggagatttgggcctgactgtcagcccgcagc	2577	Qy
6167	TGTCTGCCTTGATCAGTACTCGGCCACCGGAGAGTGTAAATGCAACACCGGCTTCAATGG	6108	Db
2576	tytyccycyatctytacacacccatyyyacaytycctatyccacaccyycttcaacy	2517	Qy
6107	CTTCGGGCGAGACTGTCAGGCCTGCCCTGGAGGACCAGATGCCCCCGTGTAATAACCGGGG	6048	Db
2516	ttcatgccagactgtcaggcctgccctggaggaccagatacaccgtgtaacaaccggg	2457	Qy
6047	GGAGCGGTGCAGCCTGGTGATACAGATCCCCAGGTGCTGCAAGGG	5988	Db
2456	yaaggotgocagaacctgtgoaccgtggtgatccaaacccccaggtgotgocatggtt	2397	Qy
5987	CCAAAGGTGTGAAGCAGAAGTGTCTCTACAACC-	5931	Db
2396	lagocaaagggggtgaagaagtgtatctacaacccgttacctttcaggaggaacg	2337	Qy
5930	TCGGGGAGTGTGGGAGCTGTGTCA	5871	Db
2336	cgatattecggggggagtgeggaagttgeatttteaeteceaaatgeceaetgaaga	2277	Qy

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                                                                   ccttctggttaatctgggattgtcgccagggctaaggagccatgttgcctggatacctgg
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/ LTAINS LATION - WHILFEWSOOTGVCECGEGFSGTACETCTEGKYGIHCDQACSCVH
/ LTAINS LATION - WHILFEWSOOTGVCECKERT FERRYCTCHAGY TGDGI TVCLEINPCLE
FOGUNGTICTAINACEISNGGCSAKADCKRTTPEDGKVCTLIAVCLTKNGGCSEFAICHNTGQ
VERTCTCKPNY IGDGFTCRGSIYQELPKNPKTSQYFFQLOEHFVKDLVGPGPFTVFAP
LSAASDEEARVKDWDKYGLMPQVLRYHVVACHQLLENLKLISNATSLOGEPIVISVS
QSTVYINNKAKIISSDIISTNGIVHIIKLLSPKULLITPKDNSGRILQNLTTLATNN
GYIKESNLIQDSGLLSVITDPIHTPVTLFWPTDQALHALPAEQODFLFNQDNKOKLKE
YLKFHVIRDAKVLAVDLPTSTAMKTLQGSELSVKCGAGRDIGDLFLNGOTCRIVQREL
LFDLGYAYGIDCLLIDPTLGGRCDTFTTFDASGEGGSVUTPSCCRWSKEKGVKOKL
YNLPFKRNLEGCRERCSLVIQIPFCCKGYFGRDCQACPGGPDAPCUNRGVCLDQYSAT
GECKCNTGFTGTACEMCWPGRFGPDCLFCGCSDHGQCDDGITGSQCLCETGWTGPSC
DTQAVLPAVCTPPCSAAATCKENNTCECNLDYEGDGFTCYVDDFCKQDNGGCAKVARC
SQKGTKYSCSCOKGYKGDGHSCTCKNTCECNLDYEGDGFTTFATASQNCGSGVVGIV
VGDGLAKGEPEQLPIDRCLQDHSCTCKVGYVGDGFSCSGLLQVLMSFPSITNFLTEV
LAYGUGGAGATMATYNQLSYAQKAKYHLCSAGWLETGRVAYPTAFASQNCGSGVVGIV
DYGPRPNKSEMMDVFCYRMKDVNCTCKVGYVGDGFSCSGLLQVLMSFPSITNFLTEV
LAYGUGGAGAGATMATYNQLSYAQKAKYHLCSAGWLETGRVAYPTAFASQNCGSGVVGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uction, 5'- & 3'-end one pass sequencing and clone selection: DNA Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="FLJ00112"
<606. .4184
                            LGKQQPENISNPLYESTTSAPPEPSYDPFTDSEERQLEGNDPLRTL"
1194 c 1203 g 1052 t
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/protein_id="BAB15793.1"
/db_xref="GI:10440526"
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/note="Start codon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="spleen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Only in DataBase (2000) In press 1 to 4575)
                                                                                                                            LAYSNSSARGRAFLEHLTDLSTRGTLFVPQNSGLGENETLSGRDIEHHLANVSMFFYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="as00112"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 4575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA to mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is not identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Okumura, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Okumura, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone:as00112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              partial cds
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	1082 1018	y 1023 cagcaatggaggatgttctacaaaggccgactgtaaaagaaccaccccaggaaaccgggt	рь
	1022 958	y 963 atgtgcggcaggattccgagggaatggaacggtctgcacagccatcaatgcctgtgagac 	рь
	962 898	8 9	Db Qy
	902 838	y 843 ctgtgacgtcggctggcgaggagtgaagtgtgacatggagatcaccacagacaactgcaa 	ОУ
	842 778	y 783 agcatgctcttgtgtccatgggagatgtagccaaggacccttgggagacggctcctgtga 	Ор
	782 718	yy 723 cttcaatgggacagcctgtgaaacctgcactgaggggaagtatggtatccactgcgacca 	ОУ
	722 658		ОУ
	662 600	603 gctggcttctttggcccacaatgccs 	ДУ
	602 540	y 544 tccgtattcatcgggtgccagccacagtgtgtgagaaccatcattacaagagcctgctg- 	Dp QA
æ	543 480		94 70
	486 420	427 attattgtgagagggagtgtggaaa 	Db Oy
	426 360	w w	ОУ
	366 300	ν ω	ОУ
	306 240	y 247 atgcaccgagagaccatgctggggttctccttacctcctttgccttctttct	ОУ
	246 180	y 187 attctacggtaccatgtggtcctgggggaaaagctcctgaagaatgacttgcataacggc 	Qу
	186 120	y 127 aacaatgaagccatcgaaaactatatcagggagaaagacaaagccacatctctaaaggaagat	Оy
	126 60	y 67 attcattacaacctggcaagtgcaatcgagtctgcagatgcttatactgtgttcgtgcca 	Оу
9;	aps	Query Match 60.0%; Score 2823.6; DB 9; Length 4575; Best Local Similarity 79.0%; Pred. No. 0; Matches 3476; Conservative 0; Mismatches 904; Indels 20; G	

2162 2098	2103 ctcagagctgagtgtgaggtgtggaactggcagtgacatcggtgagctctttctaaacga 	ОУ :		
2102 2038	2043 agactccaaggctttagcttcagacctccccaggtctgcttcctggaagaccctgcaagg	Qy :		
2042 1978	1983 cctgttcaatcaagacaacaaggacaagctgaagtcttacctgaagttccacgtgatccg 	Ωу 	-	
1918	1923 cactglcttctggcctacggacaaagccctggaagccttgccccagagcagcagagactt 	Db CY		
. io io	863 caagttgatacaggactcaggcttgctgtcagtcatcactgactccatcca			
1862 1798	1803 gggcagggttctgcaaaatcttactacagtggcagcaaaccacggatataccaaattcag 	Qy		
1802 1738	1743 ccacgttatagacaagttgctgtctcccaaaaacttgcttatcacccccaaagatgcctt	Оy		
1742 1678	1683 gttcataaacaatgaggcgaaggtcctgtccagtgacatcatcagcaccaatggcgtcat	Оy		
1682 1618	1623 cacaagtgccacgaccetccaaggagagccagtttccatctctgtctctcaggacactgt	рь .		
1622 1558	1563 ggttcttcgctatcacgtggtgggctgccagcagctgctgttggacaacctaaaagtgac 	Qy Db		
1562 1498	1503 tagctccttcaatcatgagccccggattaaagactgggatcagcagggcctcatgtccca	ДЪ		
1502 1438	1443 ggagcatgctgtccgagagcttgctggacctggccccttcaccgtgttcgcgcctttgtc	Qy Db		
1442 1378	1383 cagcatctacggggagcttcccaagaacccttcgacgtcccagtacttcttccagttgca 	Qу		
1382 1318	1323 agatcaaaggatatgtacctgcaagccagactacacgggtgatggaatcgtctgccgggg	Qу		
1322 1258	1263 tgtctgcctaacgaacaatggcggctgcagtccatttgccttctgcaactacactgagca 	Qy Db		
1262 1198	1203 ggccgtctgtaactgcttgccgaagtacactggagatggaaaggtctgcttgct	Qy Db		
1202 1138	1143 tttggagaaccatggtggctgtgacagaaatgcagagtgcacacagacag	Qy Db		
1142 1078	1083 gtgtgtgtgcaaggcaggctataccggcgacggcatcgtgtgccttgaaatcaacccgtg	Qy Db		

3302	3243 caaagaagcctgtgccaaagaagctgcgaccatagccacctacaaccagctctcctatgc	Оу
3175	3116 TGTTGGGGTGTTCCATCTACGCTCCCCACTGGGCCAGTATAAGCTGACCTTTGACAAAGC	DЬ
	183 cgtaggagtattccatctacgctccccactgggccagtacaaactgacatttgacaaag	Qy
3115	056 GGACAATGGGCAGTGCCATGCAGACGCCAAATGTGTCGACCTCCAC	B
3182	123 ggacaacggacagtgccacccagatgccagctgtgcagacctctacttccaggacacga	Qy
3055	3063 ctatgtcggggacggagtggactgtgagcctgagcagctgccgctcgaccgttgcttaca	рь
9	936 CGAGCACGCCACCTGTAAGATGACAGGCCCGGGCAAGCACAAGTGTGAGTGTAAAAGT	Db
90	003	Оу
2935	2876 GGACGGGCACAGCTGCACAGAGATAGACCCCTGTGCAGACGGCCTTAACGGAGGGTGTCA	Db
3002	gatggctacagctgcatagagatagacccctgtgcagacggtgtcaacgggggatgcc	Qy
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2012	700 UGGAATUAKAIGUAKAGITGIGGAATITICIGKAAKKAGGAKKAAKGGGAGATAAAGGG	000
88	2823 ogggatcacatgcacagtcgtggacttctgcaaacagaacaacgggggctgtgcgaaggt	Qy
2755	696 TGCTCATGCCACCTGTAAGGAGAACAACACGTGTGAGTGTAACCTGGATTATGAAGG	DЬ
2822	763 cgtgcacgccacctgtacggagaacaaccacgtgtgtgtg	Qy
2695	636 GACAGGCCCCTCGTGACACTCAGGCAGTTTT	Db
2762	703 gacagoogottogtgtgacactoccacagotgtattogcagtgtgcacacotgcttgct	Qy
2635	76	Db .
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2575	2516 GTGTGAGATGTGCCGGGGGAGATTTGGGCCCTGATGTCTGCCCTGTGGCTCAGA	Db
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2335	279 AAAGGGTGTGAAGCAGAAGTGTCTCTACAACCTGCCCTTCAAGAGGAACCTGGAAG	DЬ
2402	w	Qy
2278	219 TGCCTCGGGGGAGTGTGGGAGCTGTGTCAA	Db
2342	283 tattccggggggggtgcggaagttgcattttcactcccaaatgcccactgaagagcaagc	Qy
	15	B 5
ن د	003 +cootagotagotagotagotagotagotagotagotagota	
2222	2163 acaaatgtgcagattcatacaccggggactcttgtttgacgtggggtgtgggcctatggcat	Db Oy

4375	catggatcagttgttttaaagaatgacaacactcataagccagcc	4316	Qy
4252		4196	DЬ
4315	agaagccagcaagcaaccacagtcacggttccacggtgattcccagcccc	4256	Оу
19	CTCTGAAGAACGGCAGCTTGAGGGCAATGACCCCTTGAGGACACTGTGAGGGCCTGGACG	4136	da Vy
у F	CENTAND	ָר ס	> 5
4198	CCCtCtgtatgagacctcaggcgcggcaccccagagtcctcctgtgacccctttcacaga	4139	Qy
4075	CGGAAGAGGACATTAATGTTGCAGCTCTTGGCAAGCAGCAGCCTGAGAATATCTCGA	4016	Дb
4138	-tcagaagaggacattgatgtcttggcttttggcaagcagccccaagaatatcgcaaa	4080	Qy
4015	CTGCTTACTCCTACTTTCGGATAAACCGGGAGAACAATCGGCTTCCAGCATTTTG	3956	ф
4079	ttactcttacttccggctaaagcagcgaaccactggtttccagcgtttt	4020	Оy
3955	GCTTGGGAGCAGGGATCTTCTTTGCCATCATCCTGGTGACTGGGGCTGTTG	3896	Db
4019		3960	Qy
3895	GGGATCATTCATGTCATTTCCAGGCCTTTAAAAGCACCCCCTGCCCCCGTGA	3836	Db
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3835	GGTTTGTTGATGGAAGAGCCATTCTGCAGTGGGACATCTTTGCCTCCA	3776	Db
3899	agaccaggtttgtggatggaagatccattctgcagtgggacatcatcgccgcc	3842	Оу
3775	GCAAACGAGGCTGGGAAGCAAGCTGCTCATCACTGCCAGCCA	3716	Db
3841	tgaggactatgctgggaagccaactgctcattaccttcagccaggacca	3783	Qy
3715	ACCACCTCGCCAATGTCAGCATGTTTTTCTACAATGACCTTGTCAATG	3656	Db
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3475		3416	Db
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3355	CACAGCCTTCGCCTCCCAGAACTGTGGCTCTGGTGTGGGTTAGGGACTATG	3296	Db
3422	rcgactacgtatgcctctcagaagtgtggtgcaaacgttgttgggatcgtagactac	3363	Оу
3295	AGGCCAAGTACCACCTGTGCTCAGCAGGCTGGCTGGAGACCGGGCGGG	3236	Db
3362	cagaaggccaagtatcacctgtgctcggccggctggctgg	3303	Оy
3235		3176	Db

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REFERENCE
AUTHORS
TITLE
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HSM801377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99ttaatctgggattgtcgccagggctaaggagccatgttgcctggatacctgggggacc 4435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGTTGCCTTTAGGAACGTAAAGTCCTTTAAGCACTCAGAAGCCATACCTCATCTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTTCCTCCTCTGACCCTTT 4391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTGATCTGGGGGGTTGTTTCTGTGGGTGAGAGATGTGTTG-CTGTGCCCACCCAGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Project.

Genome Project.

This clone (DKFZp434E0321) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further

information about the clone and the sequencing project is available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Ca
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by LMU (Ludwig Maximilians University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens mRNA; cDNA DKFZp434E0321 (from AL133021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blum, H., Bauersachs, S., Mewes, Direct Submission Submitted (15-NOV-1999) MIPS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Munich/Germany) within the cDNA sequencing consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL133021.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 3642)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.mips.biochem.mpg.de/proj/cDNA/.
                                     FGRDCQACPGGPDAPCNNRGVCLDQYSATGECKCNTGFNGTACEMCWPGRFGPDCLPC
GCSDHGGCDDG1TGSGQCLCETGWTGPSCDTQAVLPAVCTPPCSAHATCKENNTCECN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann,
                                                                                                                                                          WPTDQALHALPAEQQDFLFNQDNKDKLKEYLKFHVIRDAKVLAVDLPTSTAWKTLQGS
ELSVKCGAGRDIGDLFLNGQTCRIVQRELLFDLGVAYGIDCLLIDPTLGGRCDTFTTF
DASGECGSCVNTPSCPRWSKPKQVKQKCLYNLPFKRNLEGCRERCSLVIQIPRCCKGY
                                                                                                                                                                                                                  /translation="VGEAVGTASCKCAAGFQGNGTICTAINACEISNGGCSAKADCKR
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PKTSQYFFQLDGHFVKDLVGPGPFTVFAPLSAAFDEEARVGDBCXYGLMPQVLRYHVV
ACHQLLLENLKLISNATSLQGEPIVISVSQSTVYINNKAKIISSDIISTNGIVHIIDK
LLSPKNLLITPKDNSCRILQNLTTLATNNGYIKFSNLIQDSGLLSVITDPIHTPVTLF
                    SSRPCISRTPDDLSIRGTLFVPQNSGLGENETLSGRDIEHHLANVSMFFYNDLVNGTT
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                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein"
/protein_id="CAB61358.1"
/db_xref="GI:6453578"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="DKFZp434E0321"
join(<7. .2607,2609. .3217)
/gene="DKFZp434E0321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DH10B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="strong similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="434 (synonym:
DH10B; sites NotI + SalI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="testis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="DKFZp434E0321"
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TCTCCCAAAAATTTGCTTATCACTCCCAAAGACAACTCTGGAAGAATTCTGCAAAATCTT
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NISNPLYESTTSAPPEPSYDPFTDSEEROLEGNDPLRTL*
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actacagtggcagcaaaccacggatataccaaaattcagcaagttgatacaggactcaggc 1884

2964	2905 acccaagtctcttgcagctgcaagaaaggctacaagggggatggctacagctgcatagag	Qy
2904 1977	2845 gacttotgcaaacagaacaacgggggctgtgcgaaggtcgctaagtgctcccagaaaggc 	Qy Db
28 44 1917	2785 aacaacacgtgtgttgtgtaacttgaactacgaaggtgacggggatcacatgcacagtcgtg	Оу
278 4 1857	2725 cccacagetgtattcgcagtgtgcacacctgcttgcttcgttgcacgccacctgtacggag	Qy Db
2724 1797	2665 atcacaggctccggggagtgcctctgtgaaacagggtggacagccgcttcgtgtgacact	Оy
2664 1737	2605 agatttgggcotgactgtcagcocogcagctgctccgagcatggacagtgtgatgagggg 	Оу
2604 1677	2545 ggacagtgcctatgccacaccggcttcaacgggacagcctgcgagctctgctggcatggg	Qу
2544 1617	2485 ggaggaccagatacaccgtgtaaccaaccggggcatgtgccgcgatctgtacacacccatg	Qy Db
2484 1557	2425 gtgatccaaacccccaggtgctgccatggttacttcatgccagactgtcaggcctgccct	Оу
2424 1497	2365 atctacaacccgttacctttcaggaggaacgtggaaggctgccagaacctgtgcaccgtg	ОУ
2364 1440	2305 tgcattttcactcccaaatgcccactgaagagccaagccaaagggcgtgaagaagaagtgt 	Оy
2304 1380	2245 accotaggtggcgatgtgacacttttactaccttcgatattccgggggggg	Qy Db
2244 1320	2185 cggggactottgtttgacgtgggtgtggctatggcattgactgcctactcatgaatcct 	Оy
2184 1260	2125 ggaactggcagtgacatcggtgagctctttctaaacgaacaatgtgcagattcatacac 	Оу
2124 1200	2065 gacctccccaggtctgcttcctggaagaccctgcaaggctcagagctgagtgtgaggtgt	Qу
2064 1140	2005 gacaagctgaagtettacetgaagttecaegtgateegagactecaaggetttagettea 	Oy Db
2004 1080	1945 aaagecetggaageettgeeeceagageaggaetteetgtteaateaagaeaacaag	Qy Db
1944 1020	1885 ttgctgtcagtcatcactgactccatccacccccagtcactgtcttctggcctacggac	Оу
960		Db

GG 2950 tc 4041	CTTTAAAAGCACCCCCTGCCCCGTGACCTTGACCCACACTGGCTTGGGAGCAG	2891 3982	Db
t 398	cccacggcagcaacggctgcccactctggcctggg	3922	Qy
ct 3921 CC 2890	ggaagatccattctgcagtgggacatcatcgccgccaatggaatcctccatattatttc 	3862 2831	Qy Db
at 3861 AT 2830	caactgctcattaccttcagccaggaccagctccaccaagagaccaggtttgtgga 	3805 2771	Qy Db
gc 3804 11 3C 2770	aacytotoottttacaatgacottgtcaatggtacotttotgaggactatgotgggaag 	3745 2711	Qy Db
cc 3744 	gggctaccgggaaataagagcctgtctggccgggacattgagcaccacctcactaatgt 	3685 2651	Qy Db
Jt 3684 2650	acacetgactgacetgtecatecgtggcacectgtttgtgccacagaacag 	3625 2591	Qy Db
a 36 A 25	ttcctgacagaggtgctggctttttccaagagctcagcccgaggacaggc	3565 2549	Qy
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g 3	tcgtgcagtgggaacctgctgcaggtcctcatgtccttcccctc	3505	Qy
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25 4	cgttgttgggatcgtagactacggatccagggccaacaagagtga 	 ω	Qy Db
24	gegggttgectaeeegactaegtatgeetete 	39	Qy
9 332 G 239	ccacctacaaccagctctcctatgcccagaaggccaagtatcacct 	33	Qy Db
A 23	tccccactgggccagtacaaactgacatttgacaaagccaaagaagcctgtgccaaaga 	3205 2278	Qy Db
C 3204	gatgccagctgtgcagacctctacttccaggacacgacgtaggagtattccatctacgell	31 45 2218	Qy Db
a 31 A 22	agtgccaccc AGTGCCATGC	3085 2158	Qy Db
c 3084 c 2157	acgggcccaggcaagcataagtgtgaatgtaaaagtcactatgtcggggacggagtggac 	30 2 5 2098	Qy Db
g 3024 2097	atagacccctgtgcagacggtgtcaacgggggatgccatgagcacgccacctgcaggatgllllllllll	2965 2038	Qy Db
203	TGCACAG	1978	DЬ

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REFERENCE
AUTHORS
TITLE
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VTLTHTGLGAGIFFAIILTTGAVALAAYSYFRINRRTIEFGHFESEEÐINVAALGKQQ
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KEYWORDS
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TITLE
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Best Local
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Sequence 15
AX149459
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Mammalia; Eutheria;
1 (bases 1 to 2483)
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648 c 639 g 57
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Primates;
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Pred. No. 0;
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WO0136638.
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Best Local Similarity 80.5
Matches 1468; Conservative
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a 657 c 651 g 58
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Primates;
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Pred. No. 0;
0; Mismatches
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Mammalia; Eutheria; Primates;
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Polypeptides and nucleic acids encoding
Patent: WO 0136638-A 5 25-MAY-2001;
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                                          gctacagctgcatagagatagacccctgtgcagacggtgtcaacggggggatgccatgagc
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                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res.
97191544
                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (27-AUG-1996). Osamu Ohara, Kazusa DNA Res
1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
                                                                                                                                                                                                                                                                                                                                                                                                      Ohara, O., Nagase, T., Kikuno, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Prediction of the coding sequences of unidentified human The coding sequences of 80 new genes (KIAA0201-KIAA0280) analysis of cDNA clones from cell line KG-1 and brain DNA Res. 3 (5), 321-329 (1996)
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1 (bases 1 to 6777)
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                                                    for KIAA0246 has a 1-bp deletion a
the sequence of KIAA0246"
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/product=""""
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/sex="mal-"
/product="KIAA0246 protein"
/protein_id="BAA13377.1"
/db_xref="GI:1665761"
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                                                                                                                                                 /gene="KIAA0246"
<1. .>6637
                                                                                                                                                                                           /Cell_line="KG-1"
/cell_type="myeloblast"
/tissue_type="bone marro
/clone_lib="pBluescript
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                                                         gttctggaaattcagaagaacagatgtgacaataatgacaccattattgtgagagggag
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LHFQEKRAGVFHLQATSGPYGLNESEAEAACEAOGAVLASFPQLSAAQQLGFHLCLMG
MLANGSTAHPVVFPVADCGNGRVGIVSLGARKNLSERWDAYCFRVQDVACCRCRNGCFG
DGISTCNGKLLDVLAATANESTFYGMLLGYANATQRGLDFLDELDFLDELTYKTLEVPVN
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PGTVVVSRIIVWDIMAENGIIHALASPLLAPPQPAVLAPEAPPVAAGVQAVLAAGALL
GLVAGALYLRARGKPMGFGFSAFQAEDDADDDFSPWQEGTNPTLVSVPNPVFGSDTFC
EPFDDSLLEEDPPDTQRILTVK"

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YSGNGLFCSEVDPCAHGHGGGSPHANCTKVAPGQRTCTTQCDGYWGDGELCQEINSCLI
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DGQRTCTCDTAHTVGDGLTCRARVGLELLRDKHASFFSLRLLEYKELKGDGPFTIFVP
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AFWLOPRTLPHLYRAHFLOGALFEEELARLGGGEVATLINPTTRWEIRNISGRVAVQNA
SVDVADLLATRAVULHTISQVLLPPRGDVPGGGGCLLOQLDLVPAFSLREELLQHGLUGV
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EPCPGGLGGVCSGHGQCQDRFLGSGECHCHEGFHGTACEVCELGRYGPNCTGVCDCAH
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VFHVVTGLRWQAPSGTPGDPKRTIGQILASTEAFSRFETILENCGLPSILDGPGPFTV
FAPSBEAVDSLRDGRLIYLFTAGLSKLQELVRYHIYNHGQLTVEKLISKGRILTMANQ
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                                                                                                                                                                                                                                                                                                                                Submitted (25-NOV-1999) Politz O. Benjamin Franklin Medical Centre Hindenburgdamm 30, Berlin 12200,
                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
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nmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BASE COUNT ORIGIN

24 Db 2 Вþ QY DЪ Qy Ъ Qy В Qy ÐЬ Q Ъ Matches 2066; Query Match Best Local : 3784 3664 3604 3553 3433 CTGGACTTGGTGCCTTCCAGCCTCTTCCGGGAATTGCTGCAGCACCATGGGTTGGTG 385 265 85 25 ctggagcagatgcccgactattccattttccgaggttacattattcattacaacctggca Local Similarity GCC-----CAGGGCAACAGCAGTCACCTGGACGCAGACACAGTGCGGCACCATGTG aactatatcagggagaagaaagccacatctctaaaggaagatattctacggtaccatgtg GTCCTGACGGTGGGCTCAAGTCGCTGCCTGCATAGCCACGCTGAGGCCCTGCGGGGAGAAA 3843 gttctggaaattcagaagaacagatgtgacaataatgacaccattattgtgagagggag gctccaataaactacaccaatgtggccactgataaaggagtgatccatggtctggagaaa CTGGGCCCTGCCCACTGGATCGTCTTCTACAACCACAGTGGCCAGCCTGAGGTGAACCAT GTCCTGGGGGAGGCCCTCTCCATGGAAACCCTGCGGAAGGGTGGACACCGCAACTCCCTC gtcctgggggaaaagctcctgaagaatgacttgcataacggcatgcaccgagagaccatg agtgcaatcgagtctgcagatgcttatactgtgtttcgtgccaaacaatgaagccatcgaa CCCCAGATTGAGGCTGCCACTGCCTACACCATCTTTGTGCCCACCAACCGCTCCCTGGAG Conservative 14.8%; 51.5%; 0; Pred. Pred. No. 6.9e-188; Mismatches 1823; Indels Length 7870; 125; Gaps 3783 3663 3552 3492 444 324 264 3603 144 84 384 204 15;

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Polypeptides and nucleic acids encoding
Patent: WO 0136638-A 13 25-MAY-2001;
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Pred. No. 7.2e-171;
0; Mismatches 224;
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Sequence 19
AX149463
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                   Bukaryota; Metazoa; Chordata; Craniata; Mammalla; Eutheria; Primates; Catarrhini 1 (bases 1 to 1577)
Shimkets,R.A., Lichenstein,H., Vernet,C. Polypeptides and nucleic acids encoding patent; Wo 0136638-A 19 25-MAY-2001; Curagen Corporation (US)
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                                                      Vernet, C.
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SEQUENCE, 18
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/db_xref="taxon:9606"
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Pred. No. 2e-136;
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (09-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 25, 2001 this sequence version replaced gi:8077096. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J. Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J. Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
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Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 213014 bases at least Q40 Consensus quality: 214764 bases at least Q30 Consensus quality: 215528 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 210000; agarose fp
Insert size: 216373; sum of contigs
Quality coverage: 10.2 in Q20 bases; agarose fp
Quality coverage: 9.9 in Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: M13; M77815; 44% of reads Sequencing vector: Plasmid; n/a; 56% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
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                        3322 23421: gap of 100 bp in length 23422 24529: contig of 1108 bp in length 24530 24629: gap of 100 bp 24630 24629: gap of 100 bp 24630 24629: gap of 2330 bp in length 24630 26959: contig of 2330 bp in length
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   2330
100 br
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43366 43465: gap of 100 bp
46874: contig of 3409 bp in length
46875 46974: gap of 100 bp
46975 51691: contig of 4717 bp in length
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28341. .30420
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30521. .32131
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14575: contig of 23139 bp
14575: gap of
208697: contic
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118666: contig of 66875 bp
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43365: contig of
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36716: contig of
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34170: contig of
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140: gap of 100 bp
30420: contig of 2080 bp
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 215871 TCAATGAAGACAACAAGACAAGCTGAAGCATACCTGAAGTTCCACGTGATCCGAGATA 215930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 215811 TCTTCTGGCCTACGGACAAAGCCCTCCAAGCCTTGCCTCAGGAGCAGCAGCAGGACTTCCTGT
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Best Local Similarity
Matches 166; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1928 tottotggcotacggacaaagccotggaagcottgcocccagagcagcaggacttoctgt 1987
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                                   Elhaj, C., Escotto, M., Falls, T., Ferragutto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garrer, T., Garcia, A., Guevar, W., Harris, C., Hodgson, A., Houses, A., Houloway, C., Hollins, B., Homsi, F., Howard, S., Homer, J., Hulyk, S., Hume, J., Jackson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Lewis, L.C., Kratovio, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucler, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Massey, E., Mawhiney, E., Michell, T., Mohabbat, K., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Rejas, A., Rojas, A., Rojabokan, I., Rolfe, M., Nickerson, E., Nguyen, I., Rolfe, M., Rojas, A., Rojas, A., Rojabokan, I., Rolfe, M., Nickerson, E., Martin, R., Rojas, A., Rojabokan, I., Rolfe, M., Nickerson, E., Martin, R., Rojas, A., Rojas,
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Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
Dugan, Rocha, S., Durbin, K.J., Barnhart, C., Edwards, C.C.,
Denn, A.L., Durbin, K.J., Barnhart, C., Edwards, C.C.,
Denn, A. C., Durbin, K.J., Barnhart, C., Edwards, C.C.,
Denn, A. C., Durbin, K.J., Barnhart, C., Edwards, C.C.,
Denn, A. C., Durbin, K.J., Barnhart, C., Edwards, C.C.,
Denn, A. C., Durbin, K.J., Barnhart, C., Edwards, C.C.,
Denn, A. C., Durbin, K.J., Barnhart, C., Edwards, C.C.,
Denn, A. C., Durbin, K.J., Barnhart, C., Edwards, C.C.,
Denn, A. C., Durbin, K.J., Barnhart, C., Edwards, C.C.,
Denn, A. C., Durbin, C., Durbin, C., Durbin, C.C.,
Denn, A. C., Durbin, C., Durbin, C., Durbin, C., Durbin, C.C.,
Denn, A. C., Durbin, C., Durbin, C., Durbin, C.C.,
Denn, A. C., Durbin, C., Durbin, C., Durbin, C., Durbin, C.C.,
Denn, A. C., Durbin, C., Durbin, C., Durbin, C., Durbin, C.C.,
Denn, A. C., Durbin, C., Du
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 157216)
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Homo sapiens chromosome 3 clone Rp11-54J3,
PROCRESS ***, 33 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC022277.19 GI:16117886
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47778 c 47469 g 59125 t
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/note="assembly_fragment
clone_end:T7
Ren,Y., Rives,M., Rojas,A.,
avery,G., Scherer,S., Scott,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.3%;
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Pred. No. 4.6e-32;
0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brown, M., Bryant, N.P., Buhay, C.,
Scott, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1744 others
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     Shen, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gunaratne, P., Hale, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edwards, C.C.,
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K. Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R. Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williamson, A., Wleczyk, R., Rooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Oct 14, 2001 this sequence version replaced gi:12043785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Chemistry: Dye-primer Bodipy: 15% of reads chemistry: Dye-terminator Big Dye: 85% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 150347 bases at least Q40 Consensus quality: 159720 bases at least Q30 Consensus quality: 182034 bases at least Q30 Consensus quality: 182034 bases at least Q30 Consensus quality: 175036; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 157216)
                                                                                                                                                                                                                                                                                                      Sequencing vector: M13;
                                                                                                                                                                                                                                                                                                                                                                      Center clone name: RP11-54J3
                                                                                                                                                                                                                                                                                                                                                                                              Center project name: HACM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- Genome Center
                                                                                                                                                                                                                                                                                                                                 Summary Statistics
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isa,A., Tamerisa,K.,
             estimation
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COMMENT

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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 33 contigs. The true order of the pieces

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence be preserved as soon as it is available and the accession number will 64197 64297 71247 71347 715527 75527 75627 79096 79196 83354 83354 83454 59053 58953 47023 47123 52673 52773 22905 23005 30747 $14173 \\ 14273$ 39032 30847 38932 75626: 79095: 79195: 83353: 5905 5895 3893 14272: gap of 22904: contig 471 gap o gap of contig gap of contig gap of contig gap of contig gap o gap or contig gap o: conti gap o conti gap o gap of contig of 14172 bp in length unknown of 6180 unknown of 5144 unknown of 7991 unknown of 8085 unknown of 4315 unknown of 4158 unknown of 3469 unknown of 4180 unknown of 6950 unknown length
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Best Local Similarity
Matches 166; Conserv
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gcaggatgacgggcccag
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                                                                                                             GCACAGAGATAGACCCCTGTGCAGACGGCCTTAACGGAGGGTGTCACGAGCACGCCACCT 113990
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/db_xref="taxon:9606"
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ALIGNMENTS

ABA04648 RESULT HARE; Hyaluronic Acid Receptor for Endocytosis; hyaluronan; chondroitin; chondroitin sulphate; extracellular matrix; cartilage; skin; Rat Hyaluronic Acid Receptor for Endocytosis, HARE, coding sequence vitreous 22-FEB-2002 ABA04648; ABA04648 standard; cDNA; humour; endocytic receptor; glycosaminoglycan; rat; (first entry) 4706 ВР

25-APR-2001; CDS WO200181544-A2 Rattus norvegicus. 2001WO-US13403 /partial Location/Qualifiers
1..4296 /note= /*tag= /product= "Rat HARE" "No start codon given" a

25-APR-2000; 02-NOV-2000; 2000US-199538P. 2000US-245320P.

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	gatccagggccaacaagagtgaaatgtgggatgtcttctgttaccggatgaaagatgtg	4.2	Db
3480		4	Qy
3420	acccgactacgtatgcctctcagaagtgtggtgcaaacgttgttgggatcgtagactac	w	Db
3420	acccgactacgtatgcctctcagaagtgtggtgcaaacgttgttgggatcgtagactac	3361	Qy
3360		(LI)	Db
		L.	Qy
3300	gccaaagaagcctgtgccaaagaagctgcgaccatagccacctacaaccagctctcctat	N	Db
3300	ccaaagaagcctgtgccaaagaagctgcgaccatagccacctacaaccagctctcctat	N	Оy
3240	tccatctacgctccccactgggccagtacaaactgacatttgacaaa	₩.	Db
3240	ccgtaggagtattccatctacgctccccactgggccagtacaaactgacatttgacaaa	_	Qy
3180	aggacaacggacagtgccacccagatgccagctgtgcagacctctacttccaggacacg	₩.	Db
3180	aggacaacggacagtgccacccagatgccagctgtgcagacctctacttccaggacacg		Qy
3120	cactatgtcggggacggagtggactgtgagcctgagcagctgccgctcgaccgttgctta	3061	Db
3120	actatgtcggggacggagtggactgtgagcctgagcagctgccgctcgaccgttgctta	3061	Qy
3060	atgagcacgccacctgcaggatgacgggcccaggcaagcataagtgtgaatgtaaaagt	3001	Db
3060	atgagcacgccacctqcaggatgacgggcccaggcaagcataagtgtgaatgtaaaagt	00	Qy
3000	ggggatggctacagctgcatagagatagacccctgtgcagacggtgtcaacgggggatgc	9	Db
3000	gggatggctacagctgcatagagatagacccctgtgcagacggtgtcaacggggggatgc	4	Оу
2940	gtcgctaagtgctcccagaaaggcacccaagtctcttgcagctgcaagaaaggctacaag	2881	Db
2940	togotaagtgotcocagaaaggoacccaagtctcttgcagctgcaagaaaggotacaag	2881	Оу
2880	gtgcgaag	2821	DЬ
2880	 acgggatcacatgcacagtcgtggacttctgcaaacagaacaacgggggctgtgcgaag	2821	Qy

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RESULT
ABA0467
ID ABA0
XX ABA0
XX ABA0
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DT 22-F
XXX
DE Huma
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DE Huma
XXX Chon
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                                   HARE; Hyaluronic Acid Receptor for Endocytosis; hyaluronan; chondroitin sulphate; extracellular matrix; cartilage; skin; vitreous humour; endocytic receptor; glycosaminoglycan; humo
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Best Local Similarity 79.3
Matches 3483; Conservative
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                                                                                                                                                                                                                                                                                                                               The present invention relates to sequences for rat and human HARE (Hyaluronic Acid Receptor for Endocytosis, ABA04648, ABA04652, AAM47675 and AAM47684). HARE can bind specifically to at least one of hyaluronic acid (HA, also known as hyaluronan), chondroitin (C) or chondroitin sulphate (CS). HA is an extracellular matrix component of all tissues, in particular cartilage, skin and vitreous humour. HARE is the endocytic receptor responsible for removing HA and other glycosaminoglycans from the circulation. The present sequence is the coding sequence for human maps.
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                          identifying a
nucleic acid
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attattgtgagaggggagtgtggaaagtgttcccagcaagccccctgcccactcgagaca
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                                                                 cagctgtatgtaaatgaagctccaataaactacaccaatgtggccactgataaaggagtg
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2517	Db	tagctccttcaatcatgagccccggattaaagactgggatcagcagggcctcatgtccca 1562	Qy 1503
2583	 0v	ggagcatttcgtgaaagatctggtcggcccaggccccttcactgtttttgcaccttta	1380
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2523	Qy	1. 1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.	1 4 6
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2043	Qy	atatacaacaaattccaaaaaataaaataaatctacaaaaacaatctacaataat	963
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1860	Db		780
1923	Qy	Ctataacatcacctaacaaaaaaatataaaatataacataacatcaccac	843
1800	Db		720
1863	Оу	######################################	783
1740	Db		660
1803	Qy		702
1680	Db		601
1743	Qy	gggaacggcttctgtctgggacggtgtgaatggcactggcacggca	663
1620	Db		541
1683	Qy	actaacttctttaaccoogaatacopaaacoctacoogaagaaaatatatactot 6	
1560	Db		481
1623	Qy	teeqtatteateqqqtqeeaqeeaqtqtqtqtqaqaaceateattacaaqaqeetqetq- 6	544
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2159	aaacctgcagaattgtgcagcgggagctcttgtttgacctgggtgtggc	10	Db
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2099	tcagagctgagtgtgaaatgtggagctggcagggacatcggtgacctctt.	04	Db
2162	gagctgagtgtgaggtgtggaactggcagtgacatcggtgagctctttctaaacg	10	Qy
2039	gatgccaaggttttagctgtggatcttcccacatccactgcc	æ	Db
2102	gactccaaggctttagcttcagacctccccaggtctgcttcctggaagaccctgcaag	04	Qy
97	agctgaaggagtatttgaagtttca	92	Db
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1802	cacgltaragacaagttgctgtctcccaaaaacttgcttatcacccccaaagatgcctt	74	Qy
1679	alaaacaataaggctaagatcatatccagtgatatcatcagtactaatgggattgt	62	Db
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AAF87120 standard; DNA;

3625 ВP

26-MAR-2002 (first entry)

coding sequence

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Unidentified

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16-NOV-2000;
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DV12; NOV13;
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                                                                                                                                                         This sequence encodes the NOVB protein. The invention relates to CC the NOV1-NOV16 proteins, and their coding sequences. The proteins have CC Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and CC cardiovascular activities. The sequences may be used in the prevention, CC diagnosis and treatment of diseases associated with inappropriate NOVX CC expression. They may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC supplement the patients own production of protein. They are used to CC produce NOVX proteins, by inserting the nucleic acid into a cell and CC culturing it to express the protein. The DNA may be used as DNA probes in assays to detect and quantitate the presence of similar DNAs in samples, CC and which patients may need restorative therapy. The NOVX protein may CC NOVX and in assays to identify modulators of NOVX expression and activity. The anti-NOVX Abs are used for detecting the presence of NOVX in samples. Disorders that may be prevented, diagnosed CC expression and activity. The anti-NOVX Abs are used for detecting the CC presence of NOVX in samples. Disorders that may be prevented, diagnosed CC NOV7, NOV9-11 and NOV13-16 have casein kinase II phosphorylation sites C characteristic of serincy/threonine kinases, and are used to treat kinase-related disorders (e.g. Peutz-Jeghers syndrome, cellular CC the epidermal growth factor (EG)-like super family and are involved in, cell structure and motility and protein management, and are used to treat cancers, inflammatory disorders, immune disorders and cc cellular adhesion disorders (NOY6-10 are homologous to FGE-11 ke
                                                                                        Query Match
Best Local S
Matches 1469
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                                                                                                                                   cardiovascular disease; hypertrophic cardiomyopathy; marfan therapy; NOV1; NOV2; NOV3; NOV4; NOV5; NOV6; NOV7; NOV8; NOV11, NOV11; NOV13; NOV14; NOV15; NOV16; ds.
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This sequence encodes the NOV6 protein. The invention relates to the NOV1 NOV16 proteins, and their coding sequences. The proteins have CC the NOV1 NOV16 proteins, and their coding sequences. The proteins have CC victostatic; contraceptive; antiinflammatory; immunomodulatory; and CC cardiovascular activities. The sequences may be used in the prevention, CC diagnosis and treatment of diseases associated with inappropriate NOVX CC expression. They may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of protein by expressing inactive proteins or to CC supplement the patients own production of protein. They are used to CC supplement the patients own production of protein. They are used in CC assays to detect and quantitate the presence of similar DNAs in samples, CC and which patients may need restorative therapy. The NOVX protein may CC also be used as antigens in the production of antibodies (Abs) against CC NOVX and in assays to identify modulators of NOVX expression and crivity. The anti-NOVX Abs and antagonist are used for detecting the CC expression and activity. The anti-NOVX Abs are used for detecting the CC expression and activity. The anti-NOVX Abs are used for detecting the CC expression and activity. The anti-NOVX Abs are used for detecting the CC expression and activity. The NOVX protein may be prevented, diagnosed and/OV7 NOV9-11 and NOV13-16 have casein kinase II phosphorylation sites Characteristic of serine/threonine kinases, and are used to treat CC kinase-related disorders (EGF) like super family and are involved in, e.g. regulation of cell development, apoptosis, cell adhesion, growth cell creditions and accivity and protein management, and are used to treat cancers, inflammatory disorders, immune disorders and cc elibrillar adhesion disorders. NOV6-10 are homologous to EGF-like control of cell development, and protein management, and are used to treat cardiovascular disease e.g. fibrillar an
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This sequence encodes the NOV2 protein. The invention relates to the NOV1 NOV16 proteins, and their coding sequences. The proteins have CC the NoV1 NoV16 proteins, and their coding sequences. The proteins have CC vytostatic; contraceptive; and tinflammatory; immunomodulatory; and CC cardiovascular activities. The sequences may be used in the prevention, CC diagnosis and treatment of diseases associated with inappropriate NOVX CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of protein by expressing inactive proteins or to cc supplement the patients own production of protein. They are used to CC supplement the patients own production of protein. They are used to CC ulturing it to express the protein. The DNA may be used as DNA probes in CC assays to detect and quantitate the presence of similar DNAs in samples, CC and which patients may need restorative therapy. The NOVX protein may cc also be used as antigens in the production of antibodies (Abs) against CC NOVX and in assays to identify modulators of NOVX expression and cctivity. The anti-NOVX Abs and antagonist are used for detecting the expression and activity. The anti-NOVX Abs are used for detecting the CC presence of NOVX in samples. Disorders that may be prevented, diagnosed CC and/or treated vary depending on the NOVX protein. NOV1, NOV3, NOV5.

CC characteristic of serine/threonine kinases, and are used to treat CC kinase-related disorders (e.g. Peutz-Jeghers syndrome, cellular chesion, cell development, apoptosis, cell adhesion, growth in the epidermal growth factor (ECF)-like super family and are involved in, cell creations, and are used to treat cancers, inflammatory disorders, immune disorders and cellular adhesion disorders. NOV6-10 are homologous to ECF-like contents and are used to treat cardiomyopathy, long-OT syndrome and marfan syndrome.
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Cytostatic; contraceptive; and their cooling sequences. The proteins have CC Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and contraceptive; antiinflammatory; immunomodulatory; and CC diagnosis and treatment of diseases associated with inappropriate NOVX CC expression. They may be used to treat disorders associated with decreased contract the activity of protein by expressing inactive proteins or to compression by rectifying mutations or deletions in a patient's genome contract the patients on production of protein in a patient's genome contract the patients of the production of protein into a cell and contract the protein system of the nucleic acid into a cell and contract the protein of protein into a cell and contract and quantitate the presence of similar DNAs in samples, and which patients may need restorative therapy. The NOVX protein may cativity and in assays to identify modulators of NOVX expression and contract into a cell and contract into a case in the Novx protein. Nov1, Nov3, Nov5, cell and contract into a case in the Novx protein would are homologous to treat cancers, inflammatory and are family and are involved in, cell are decreased into a cell adhesion disorders. Nov6-10 are homologous to EGF-like conformed are used to treat cardiovopathy. Inda-Or syndrome and marfan syndrome e.g..
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29-NOV-1999;
08-MAR-2000;
16-NOV-2000;
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                                                                                            hypertrophic cardiomyopathy,
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specification descr.'
WF-HABP, WF-"

WF-HABP, OE-HABP,

equence encodes a hyaluronan binding protein. The describes four hyaluronan binding protein, known as ABP, OE-HABP, and BM-HABP. The polypeptides are useful diseases such as proliferative conditions, metastasis,

proliferative

HABP, OE-HABP, and diseases such as p

metastasis,

457pp;

English.

hyaluronan-binding proteins, known as full-length WF-HABP, WF-HABP and BM-HABP, useful for treating proliferative conditions, astasis, inflammation, ischemia, arthritis and multiple scleros

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WF-HABP

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dysfunction; immune surveillance dysfunction;
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/transl_except= (pos: 6341..6343, aa: Xaa)
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                                                      ating proliferative conditions arthritis and multiple sclero:
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The present sequence encodes a hyaluronan-binding protein. specification describes four hyaluronan-binding protein, k

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Human ORFX ORF1928 08-FEB-2001

polynucleotide sequence

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02-APR-1999;
05-APR-1999;
30-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antihetensive; dermatological; immunosuppressive; antihinflammatory; antibacterial; antiviral; antithugal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORRY-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lupus arrive entering severe combined immunodefficiency (COTN) and storage and storage and storage and storage and storage and storage and storage.
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                                3263 aagctgcgaccatagccacctacaaccagctctcctatgcccagaaggccaagtatcacc 3322
                                                                                                                                                                                                                                                                                                                                                                               allergies, aplastic anaemia, burns, wounds, bone and cartilage damage. nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                  Sequence
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08-MAR-2000;
16-NOV-2000;
               Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NOVX expression. They may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins or to supplement the patients own production of protein. They are used to produce NOVX proteins, by inserting the nucleic acid into a cell and culturing it to express the protein. The DNA may be used as DNA probes in assays to detect and quantitate the presence of similar DNAs in samples, and which be activities and described by the protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardiovascular; casein kinase II phosphorylation site; contraception; serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation; epidermal growth factor; cell development; apoptosis; cell adhesion;
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                                                                                                                                                                                                                                                                                                   sequence encodes the NOV7 protein
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2000US-0715417.
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need restorative therapy. The NOVX protein may
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Best Local Similarity
Matches 830; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOV7, NOV9-11 and NOV13 16 have casein kinase II phosphorylation sites characteristic of serine/threonine kinases, and are used to treat kinase-related disorders (e.g. Peutz-Ueghers syndrome, cellular proliferation and contraception). NOV2-3, NOV6 and NOV8 are homologous the epidermal growth factor (EGF) like super family and are involved in e.g. regulation of cell development, apoptosis, cell adhesion, growth migration, cell structure and mottlity and protein management, and are used to treat cancers, inflammatory disorders, immune disorders and used to treat cancers, inflammatory disorders, immune disorders and
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                   tgtgcagattcatacaccggggactcttgtttgacgtgggtgtggcctatggcattgact
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29-NOV-1999;
08-MAR-2000;
16-NOV-2000;
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 P-PSDB;
                                        Shimkets RA,
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                                                                   (CURA-) CURAGEN CORP
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2001-648134/74
DB; AAB83366.
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2000US-187844P.
2000US-0715417.
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                                        Lichenstein
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Complement the patients own production of patient's genome that affect the activity of protein by expressing inactive proteins or to consume the patient's own production of protein. They are used to produce Novy proteins, by inserting the nucleic acid into a cell and continue Novy proteins, by inserting the nucleic acid into a cell and continue Novy protein may need restorative therapy. The Nova protein may cand which patients may need restorative therapy. The Nova protein may cand which patients may need restorative therapy. The Nova protein may cativity. The anti-Nova has and antiponist are used to down regulate convavand in assays to identify modulators of Nova expression and cativity. The anti-Nova has are used for detecting the capteristic of semines. Disorders that may be prevented, diagnosed and/or treated vary depending on the Nova protein. Nova, Nova, Novy-11 and Novi3-16 have casein kinase II phosphorylation sites characteristic of serine/threonine kinases, and are used to treat ckinase-related disorders (e.g. Peutz Jephers syndrome, cellular conjection, cell structure and motility and protein management, and are used to treat cancers, inflammatory disorders, immune disorders and cellular adhesion disorders. Nov6-10 are homologous to EGF-like conventions and are used to treat cardinary cardinary disorders, and are disorders e.g. hypertrophic cardinary disorders and marfan syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the NOVI-NOV16 proteins, and their coding sequences. The proteins have Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NOVX expression. They may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and
hypertrophic cardiomyopathy, long-QT syndrome
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Sequence 1577 BP; 424 A; 410 C; 342 G; 401 T; 0 other;

Matches

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  New hyaluronan-binding proteins, known as full-length WF-HABP, OE-HABP and BM-HABP, useful for treating proliferative condition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "hyaluronan-binding protein" /product= "hyaluronan-binding protein" /transl_except= (pos: 1102..1104, aa: Xaa) /transl_except= (pos: 1255..1257, aa: Xaa) /transl_except= (pos: 1297..1299, aa: Xaa) /note= "Xaa is an unspecified amino acid"
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Best Local Simi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multiple sclerosis; rheumatoid arthritis; ulcerative colitis; acquired immunodeficiency syndrome; AIDS; cardiovascular disorder; myocardial ischaemia; wound healing; neurological disorder; parkinson's disease; Alzheimer's disease; cerebral anoxia; epilepsy; viral infection; bacterial infection; fungal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preservative; immunogen; antibody; bone cancer; adrenal cancer
bone marrow cancer; breast cancer; gastrointestinal cancer;
liver cancer; lung cancer; urogenital cancer; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS00854 standard; cDNA;
                                       Twenty nine nucleic acid molecules encoding human cancer associated proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases -
                                                                                                                                                                                                      03-SEP-1999;
06-OCT-1999;
                                                                                                                                                                                                                                                30-AUG-2000;
                                                                                                                                                                                                                                                                             15-MAR-2001.
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                                                                                                                                              Roschke
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DB; AAU00893.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggaagttgcttccggcccactcaggcctcagcctcatcatcagtgacgcaggccctgaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA clone HLMIT84 encoding cancer related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer related protein; HLMIT84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                  2000WO-US23794
                                                                                                                                                                           GENOME SCI INC
                                                                                                                                                                                                      99US-0152296.
99US-0158003.
                                                                                                                                                                                                                                                                                                                                   /product= "Cancer related
/partial
/note= "No start codon"
                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                383;
             427pp;
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               English
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Page

RESULT 1
AAS62772
ID AAS6
XX
AC AAS6
XC AAS6
XX
DT 14-F
XX
CDR CDNA

AAS62772 standard; cDNA;

722

ВР

cDNA sequence

#559 encoding novel human secreted

protein.

14-FEB-2002

(first entry)

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        increase or decrease storage capabilities. The polynucleotide are useful for chromosome identification. The nucleic acids, protein, antibodies, agonists and antagonists are useful in the diagnosis, treatment and prevention of cancer (e.g. cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital), immune disorders (e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   colitis, acquired immunodeficiency syndrome, AIDS), cardiovascular disorders such as myocardial ischaemias, wound healing, neurological diseases (e.g. Parkinson's disease, Alzheimer's disease, cerebral and and epilepsy) and infectious diseases such as viral, bacterial, funga and parasitic infections. Numerous examples of each type of disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides can also be used as a food additive or preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence encodes a novel Human cancer related protein. polynucleotides and polypeptides are useful for preventing, treating or ameliorating a medical condition in e.g. humans
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gttg-ctgtgcccacccagtacagcttcctcctctgacccttt
                      gttgcctggatacctgggggacctccacctcctctgagcctat 4455
                                                                                 cagaagccatacctcatctctctggctgatctgggggttgtttctgtgggtgagagatgt
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Pred. No. 1.2e
0; Mismatches
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Which encode human secreted proteins. The cDNA sequences have been

derived from a variety of human tissues. The invention also provides

a method for producing proteins from these polynucleotide sequences.

The proteins are useful for identifying compounds that modulate their

cativity and production, and the cell is also useful for identifying

compounds that modulate expression of the polynucleotide sequences

cuseful for treating diseases such as hyperproliferative disorders

cuseful for treating diseases

cuseful for treating diseases

cuseful for identifying

cuseful modulate expression of the polynucleotide sequences

cuseful for treating diseases

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cuseful for 
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Best Local Similarity 60.9%;
Matches 231; Conservative
4377 gttaatctgggattgtcgccagggctaaggagccatgttgcctggatacctgggggacct 4436
                                                                                                                                                                                                                                                                                                                                                                                                                       4140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding secreted proteins useful for treating e.g. asthma, HIV and Crohn's disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 358; 391pp; English.
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                                                                                                                                                                                                                                                          294 tctgaagaacggcagcttgagggcaatgaccccttgaggacactgtgagggcctggacgg
                                                                                                                                                                                                                                                                                       cctggagaacaggatctggaggaccatcttggggggcactg---cggtcctgacat 4256
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                                                       agttgccttttaggaacgtaaagtcctttaagcactcagaagccatacctcatctctctg
                                                                                  gagatgccagccatcactcactgccacctgggccatcaactgtgaattctcagc---acc 410
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Db 471 gctgatctgggggttgtttctgtgggtgagagatgtgttg-ctgtgcccacccagtacag 529

Oy 4437 ccacctccttgagcctat 4455
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Search completed: June 17, 2002, 16:44:47 Job time: 9872 sec

Вb

530 cttcctcctctgacccttt 548

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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4706
        GenCore version
Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
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US-08-282-141-1

US-08-288-797-1

PCT-US95-08414-1

US-07-878-960-1

US-07-878-960-1

US-08-246-534-5

US-08-465-500-5

US-08-465-500-5

US-08-346-126-5

US-08-346-126-5

US-08-346-128-5

US-08-346-128-5

US-08-346-128-5

US-08-346-128-7

US-08-893-828-5

PCT-US90-03747-1

US-08-426-627-1

US-08-225-477B-1
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US-08-242-097-1
US-08-206-695-1
US-08-001-078A-2
US-08-463-218-2
PCT-US94-00253-2
US-08-232-463-14
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TELEFAX: 212-737-3528 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

1:

LENGTH: TYPE: n

1414 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:

NAME/KEY:

CDS

CELL TYPE:

Fibroblast FS-4

ORIGINAL SOURCE: TOPOLOGY: 1 MOLECULE TYPE:

ORGANISM:

Homo sapiens

CDNA

NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: VII
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212.628-5197

VILCEK=1

FILING DATE:
ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION DATA:
APPLICATION NUMBER:

US/07/642,312

APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435

US/08/024,868

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:

28 37 0.8 1520 5 PCT-US95-0435-1 29 36.4 0.8 3250 1 US-08-192-632-1 30 36.4 0.8 3250 1 US-08-192-632-1 31 36.4 0.8 3250 1 US-08-710-676-1 32 36.4 0.8 3250 3 US-09-099-002B-1 33 36.4 0.8 3250 5 PCT-US93-06080-1 34 36.2 0.8 289 4 US-09-07-005-17 35 36.2 0.8 289 4 US-09-244-796-17 36 36.2 0.8 18609 4 US-08-943-731-1 37 36 0.8 975 6 5340934-10 38 34.6 0.7 2447 2 US-09-244-969-14 39 34.4 0.7 3709 4 US-09-11684-3 42 33.8 0.7 4411529 4 US-09-103-940A-1 43 33.2 0.7 198 1 US-08-30-108-16 45 33.2 0.7 198 5 PCT-US95-11081-6				C						C			C	ი	C	С	C	
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0 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8
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ALIGNMENTS

RESULT 1 US-08-024-868-1 Sequence 1, Applic Patent No. 5386013 GENERAL INFORMATION: NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: Browdy and Neimark STREET: 419 Seventh Street, NW APPLICANT: Lee, Tae HO APPLICANT: Wisniewski, Hans Georg APPLICANT: Vilcek, Jan TITLE OF INVENTION: Cytokine-Indus TITLE OF INVENTION: Coding Therefo STREET: 419 Sevent CITY: Washington STATE: DC COUNTRY: US ZIP: 20004 Application US/08024868 Cytokine-Induced Protein, Coding Therefor and Uses: 2 n, TSG-6, Thereof DNA

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                           ATTORNEY/AGENT INFORMATION:

NAME: BROWDY ROGET L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: LEE26/VILCEK=1B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-628-5197

TELEPHAX: 212-737-3528

INFORMATION FOR 550 ID NO: 1:

SEQUENCE CHARACTERISTICS:
                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, VE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,097
FILING DATE: 13-WAY-1994
CLASSIFICATION 435
ATTORNEY/AGENT
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Matches 171; Conserv
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Patent No. 5846763
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Best Local
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APPLICANT: Wisns
APPLICANT: Vilce
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ZIP: 20004
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12: Browdy and Neimark

419 Seventh Street, N.W., Suite 300
ashington
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Newski, Hans Georg
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2.5e-10;
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US-09-206-695-1
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; LOCATION: 69..899
; OTHER INFORMATION:
US-08-242-097-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09206695 Patent No. 6210905
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Best Local Similarity
Matches 171; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0/
APPLICATION NUMBER: 13-MAY-1994
                           FILING DATE: 13-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3248
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TITLE OF INVENTION: Cy
TITLE OF INVENTION: Th
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
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                                                                                                                 CLASSIFICATION:
                                                                                                                                   FILING DATE
                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                               20004
          BROWDY, Roger RATION NUMBER:
                                                                                                                                                                                                                                                                                                                               419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wisniewski, Hans Georg
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: 25,618
                                                                            US/08/242,097
                                                                                                                                                   US/09/206,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 70.8; DB 2;
Pred. No. 2.5e-10;
0; Mismatches 167;
                                                                                                                                                                                                                                                                                                                               Suite 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-206-695-1
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Best Local Similarity
Matches 171; Conserv
                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08001078A Patent No. 5872094
                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Goetinck, Paul F.

APPLICANT: Tondravi, M., Mebrdad

APPLICANT: Binette, Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212-737-3528 INFORMATION FOR SEQ ID NO: 1:
ZIP: VALVE
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 69..899
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELL TYPE:
                                                                                                                                 CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212-628-5197
TELEFAX: 212-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: LEE26/VILCEK=1B
                                                                                                COUNTRY:
                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctacgtatgcctctcagaagtgtggtgcaaacgttgttggggatcgtagactacggatcca 3427
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                                                                                                                                                     60 STATE STREET, Suite
                                                                                                  USA
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FS-4
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                                                                                                                                                                                                                        METHODS FOR PROMOTING CARTILAGE MATRIX FORMATION
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                                                                                                                                                     510
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
SENGTH: 1400 base pairs
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Goetin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/001
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                      APPLICANT: Tondravi,
APPLICANT: Binette,
TITLE OF INVENTION:
TITLE OF INVENTION:
            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 05-JUNE-1
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                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3406
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PRIOR APPLICATION DATA:
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                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                    STREET: 60 STON
                                                                  SOFTWARE:
                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                      021.09
                                                                                                                                                                                                                                                                                                                                                                                              5986052
                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08463218
                                                                                                                                                                                      Massachusetts
                                                                                                                                                                                                                    60 STATE STREET, Suite 510
                                                                                                                                                                    USA
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(617) 227-5941
                                                                                                                                                                                                                                                                                                    Binette, Francois
VENTION: METHODS FOR PROMOTING CARTILAGE MATRIX
                                                                                                                                                                                                                                                                                                                                        Tondravi, Mehrdad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                  ASCII text
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                                                                                                                                                                                                                                        LAHIVE & COCKFIELD
                                                                                                                Floppy disk
                05-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.3%;
52.7%;
                                                                                                                                                                                                                                                                                          FORMATION
                                US/08/463,218
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Pred. No. 3.3e-07;
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APPLICATION NUMBER: US 08/001,078 FILING DATE: 06-JAN-1993 ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER:

MGP-008DV

Myers, Paul L.

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PCT-US94-00253-2
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Matches
                                                                                                                                   APPLICATION NUMBER: US 08/0
FILING DATE: 06-JAN-1993
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 base pairs
TYPE: nucleic acid
 Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9400253 GENERAL INFORMATION:
                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         APPLICATION NUMBER: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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Local Similarity 52.7%;
hes 157; Conservative
                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII (text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                        STRANDEDNESS:
                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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 1.3%;
ilarity 52.7%;
Conservative
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Score 60; DB 5; L
Pred. No. 3.3e-07;
0; Mismatches 135;
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Pred. No. 3.3e-07;
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                                   Length 1400;
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                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                            APPLICATION NUMBER: EP 9.
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                     IMMEDIATE SOURCE:
                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKURER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
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                                      STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
CLONE:
                                                                           TYPE:
                                                                                                                                                                  TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                           nucleic acid
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Matches 52; Conservative
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                                                                                                                                                                                                                                                      ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIKG SYSTEM: PC-DOS/MS-DOS
              NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
                                                             ATTORNEY/AGENT INFORMATION:
BENT, Stephen A.
                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SCHEIFLINGER, APPLICANT: FALKNER, F. G.
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                                                                                                                                                                                                                                                                                                                                                                         STREET: 100.
                                                                                                 FILING DATE:
APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                     APPLICATION NUMBER:
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1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                        PatentIn Release #1.0,
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(703)836-9300
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                                   30472/114 IMMU
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)2; Mismatches 215;
                                                                                                                                                                                                                                                                                                                                                                                                            Suite
                                                                                                                                                                                                                                                        Version
                                                                                                                                                                                                                                                        #1.25
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US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                              US-08-225-477B-2
                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08225477B Patent No. 5635370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.9%; Score 43.4; DB Best Local Similarity 3.6%; Pred. No. 0.054; Matches 14; Conservative 212; Mismatches
                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4319
                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" 1.44 Mb diskette
                                                                                                                                                                                                                                                                                APPLICANT: Susan Hockfield
APPLICANT: Diame M. Jaworski
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: luronan-Binding Pro
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           APPLICATION NUMBER: US/OFILING DATE: April 8, 19
ATTORNEY/AGENT INFORMATION:
                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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TELEX: 8
                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                           SOFTWARE:
                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                      CITY: Stamford
STATE: CT
                                                                                                                                                                                                                     STREET:
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Mary M. Krinsky
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                                                                           Word Processor
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6 Bedford Street
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Best Local Similarity
Matches 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9504353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                         APPLICATION NUMBER: 08/2:
FILING DATE: April 8, 199
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                           SOFTWARE: Word Processor CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3394 gcaaacgttgttgggatc 3411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3274 atagccacctacaacctacctctctttgcccagaaggccaagtatcacctgtgctcggcc 3333
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                                                                                                            FILING DATE: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" 1.44 Mb diskette
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: St. Onge
                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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TELECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Susan Hoc
APPLICANT: Diane M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE: cat cortex
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                                                                                                                                                                           OPERATING SYSTEM:
SOFTWARE: WORD PI
                                                                                                                                                                                                                                                                                                          CITY: Stamford
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REFERENCE/DOCKET NUMBER: 1:
                                REGISTRATION NUMBER:
                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                             ZIP:
                                                                                                                                                                                                                                                                             COUNTRY:
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                                               NAME:
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                                            Mary M. Krinsky
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986 Bedford Street
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luronan-Binding Protein
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               1751-P0004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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US-08-340-428B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                            FILING DAYL.
CLASSIFICATION: 514
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/922,911
TTING DATE: 03 August 1992
TTING TON: 514
TTING TON: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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TELEFAX: 203-327-1096
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MARGOLIS, Richard APPLICANT: RAUCH, Uwe APPLICANT: MARGOLIS, Renee K.
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                 ATTORNEY/AGENT INFORMATION: NAME: Browdy, Roger L.
                                                                                                                                                                                           SOFTWARE: PatentIn Relaction DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3394
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                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
            NAME: Browdy, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                        ZIP:
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                                                                                                                                                                                                                                                                                                                                                                         E: Browdy and Neimark
419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                     U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Richard U.
                                                                                                                                                          5648465ember 1994
                                                                                                      07/922,911
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Margolis=1A
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Pred. No. 0.092;
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TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO: 1:

202-737-3528

TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197

SEQUENCE CHARACTERISTICS:

LENGTH:

5191 base pairs

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Best Local Similarity
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,911
FILING DATE: 03-AUG-1992
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MARGOLIS, Renee K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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LOCATION:
                             TELEPHONE:
                                                                  REFERENCE/DOCKET NUMBER: Ma
                                                                               NAME: Townsend, Guy K
REGISTRATION NUMBER:
                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 03-AUG
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STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                     20004
                                                                                                                                                                                                                                                                                                                                                    D.C
                                                                                                                                                                                                                                                                                                                                                                                  419 Seventh Street, N.W
                 : 202-628-5197
202-737-3528
                                                                                                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAUCH, Uwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MARGOLIS, Richard U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                             PCT/US93/07306
                                                              Margolis=1A PCT
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                                                                                                                                                                                                                                 Version #1.25
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RESULT 1:
5180808-1
RESULT 14
US-08-282-141-1
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; APPLICANT: RUOSLAHTI, ERKKI I.
TITLE OF INVENTION: VERSICAN CORE PROTEIN, NUCLEIC ACID
; SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROBES, ANTI-VERSI
; ANTIBODIES, AND METHODS OF DETECTING THE SAME
; NUMBER OF SEQUENCES: 4
; NUMBER OF SEQUENCES: 4
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; LOCATION:
PCT-US93-07306-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 110; Conserv
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Best Local
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LENGTH: 5191 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/
FILING DATE: 27-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 8224
                                                                                         acgtatgcctctcagaagtgtggtgcaaacgttgttgggatcgtag
                                                                                                                                                                                                                            gcctgtgccaaagaagctgcgaccatagccacctacaacctagctctcctatgcccagaag 3309
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                                                                     cgggctcccagagtaggctgttatggagataagatgggaaaggcag
                                                                                                                                      gatggatttgagcagtgtgacgcaggctggctggctgatcagactgtcagatatcccatc 896
                                                                                                                                                                                                         gcttgtttggacgttggggcagtcatagcaactccagagcagctctttgctgcctatgaa
                                                                                                                                                                                                                                                                               gtgtttcactacagggcggcaaccagcaggtacacactgaattttgaggctgctcagaag
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                                                                                                                                                            gccaagtatcacctgtgctcggccggctggctggagagtgggcgggttgcctacccgact 3369
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48.78;
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Pred. No. 0.43;
0; Mismatches 116
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Sequence 1, Application US/08282141

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Matches
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: APPLICANT:
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CORRESPONDENCE ADDRESS: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2461 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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MEDIUM TYPE: Floppy disk
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2878 aaggtcgctaagtgctcccagaaaggcacccaagtctcttgcagctgcaagaaaggctac 2937
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                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                 APPLICANT: Purchio, APPLICANT: LeBaron,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2938 aagggggatggctacagctgcatagagatagacccctgtgcagac 2982
                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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CITY: Thousand Oaks
STATE: California
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 86; Conserv
                                                                                                                                 STREET: 620 Newport CITY: Newport Beach STATE: CA
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                                                                                              COUNTRY: U. ZIP: 92660
                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                      E: Knobbe, Martens, Olson and Bear 620 Newport Center Drive, Sixteenth Floor
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Manfioletti, Guidalberto
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Avanži, Giancarlo
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                                                                                                                                                                                                                                                                   Anthony F. Richard
                                                                                                                                                                                                                                                   Factor to Grow Tissue Ex Vivo
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                                                                                                                                             Query Match 0.8%;
Best Local Similarity 62.8%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                            1922 tcactgtcttctggcctacggacaaagccctggaagccttgcccccagagcagcagcaggact 1981
                                                                                                                                                                                                                                                           MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: TI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                   1982 tcctgttcaatcaagacaacaaggacaagctgaa 2015
                                                                      413 TCACCATCTTCGCCCCTAGCAACGAGGCCTGGGCCTCCTTGCCAGCTGAAGTGCTGGACT 472
473 CCCTGGTCAGCAATGTCAACATTGAGCTGCTCAA 506
                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Israelsen, Ned A. REGISTRATION NUMBER: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                          2049 base pairs
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Gaps

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Search completed: June 17, 2002, 16:36:14 Job time: 11744 sec

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Result
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1318.5
1264.5
1209.5
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ALIGNMENTS

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Key Domain Hyaluronan-binding protein WF-HABP; OE-HABP; BM-HABP; proliferative condition; metastasis; inflammation; ischemia; host defence dysfunction; immune surveillance dysfunction; arthritis; A human hyaluronan-binding protein, designated WF-HABP 03-OCT-2000 Domain Domain Domain Domain Domain Domain Homo sapiens multiple sclerosis; autoimmunity; immune dysfunction; allergy (first 375..386 ~~re= "EGF-like t /note= " 943..954 551..564 /note= "EGF-like type 2 /note= "I 514..523 /note= "| 508..521 /note= "EGF-like type 2 Location/Qualifiers 344..353 /note= /note= entry) "cytochrome P450 cysteine haem-iron ligand binding domain" "EGF-like type 1 domain" "EGF-like type 2 "cytochrome "cytochrome P450 binding domain" type 1 domain" cysteine domain" domain" domain" haem-iron ligand

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The present sequence represents a hyaluronan-binding protein. Specification describes four hyaluronan-binding protein, know WF-HABP, WF-HABP, OB-HABP, and BM-HABP. The polypeptides are for treating diseases such as proliferative conditions, metas
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cc and which patients may need restorative therapy. The NOVX protein may calso be used as antigens in the production of antibodies (Abs) against convex and in assays to identify modulators of NOVX expression and cativity. The anti-NOVX Abs and antagonist are used to down regulate cexpression and activity. The anti-NOVX Abs are used for detecting the presence of NOVX in samples. Disorders that may be prevented, diagnosed and/or treated vary depending on the NOVX protein. NOVI, expression by rectifying mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins or t supplement the patients own production of protein. They are used to produce NOVX proteins, by inserting the nucleic acid into a cell and culturing it to express the protein. The DNA may be used as DNA probes i assays to detect and quantitate the presence of similar DNAs in samples. Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevention diagnosis and treatment of diseases associated with inappropriate NOVX used to treat cancers, inflammatory disorders, immune disorders and cellular adhesion disorders. NOV6-10 are homologous to EGF-like fibrillin proteins and are used to treat cardiovascular disease e.g. hypertrophic cardiomyopathy, long-QT syndrome s sequence is the NOV8 protein. The invention relates to NOV1-NOV16 proteins, and their coding sequences. The proteins have They may be used to treat disorders associated with and marfan syndrome in the prevention, decreased ö

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Cytostatic; continceptive; antiniflammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NOVX expression. They may be used to treat disorders associated with decrease expression by recitiying mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins or supplement the patients own production of protein. They are used to produce NOVX profeins, by inserting the nucleic acid into a cell and culturing it to express the protein. The DNA may be used as DNA probes assays to detect and quantitate the presence of similar DNAs in samples and which patients may need restorative therapy. The NOVX protein may
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29-NOV-1999;
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16-NOV-2000;
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NNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIE
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                                         DASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKY
                                                                                                                                                                                                                                                             RFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVHATCTE
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                                                                                                                                                                                                                                                                                                                                                           VIQTPRCCHGYEMPDCQACPGGPDTPCNNRGMCRDLYTPMGQCLCHTGENGTACELCWHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALAS
                                                                                  idpcadgInggchehatckmtgpgkhkceckshyvgdgIncepeqIpidrclqdngqcha
                                                                                                                                                            nntcecnldyegdgitctvvdfckqdnggcakvarcsqkgtkvscscqkgykgdghscte
                                                                                                                                                                                                                                          rfgpdclpcgcsdhgqcddgitgsgqclcetgwtgpscdtqavlsavctppcsahatcke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             llsvitdpihtpvtlfwptdqalhalpaeqqdflfnqdnkdklkeylkfhvirdakvlav
                                                                                                                       IDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDCEPEQLPLDRCLQDNGQCHP 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins and are used to treat cardiovascular disease e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiomyopathy, long-QT syndrome and marfan syndrome
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Pred. No. 6.3e-175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A human hyaluronan-binding protein,
               1068
                                                                                                                                                                                                                                                The present sequence represents a hyaluronan binding protein. The specification describes four hyaluronan binding protein, known as we-pecification of the polypeptides are useful for treating diseases such as proliferative conditions, metastasis, for treating diseases such as proliferative conditions, metastasis,
                                                                                                                                                                                                                                                                                                                           Claim 11; Fig
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                                                                                                                                                                                                                      inflammation, ischemia, host defedysfunction, arthritis, multiple
                                                                                                                                                                                                                                                                                                                                                       metastasis, inflammation, ischemia, arthritis and multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                   New hyaluronan-binding proteins, known as full-length WF-HABP, WF-HABP, OE-HABP and BM-HABP, useful for treating proliferative conditions,
                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
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            RSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYAS
                                         mtgpgkhkceckshyvgdglncepeqlpidrclqdngqchadakcvdlhfqdttvgvfhl
                                                                       MTGPGKHKCECKSHYVGDGVDCEPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHL 1067
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280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sclerosis; autoimmunity; immune dysfunction; allergy.
                                                                                                                                                                             353
                                                                                                                                                                                                          and allergy
                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               condition; metastasis; inflammation;
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351
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                                                                                                     Mismatches
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expression. They may be used to treat disorders associated with decreexpression by rectifying mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins of

Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevendingnosis and treatment of diseases associated with inappropriate

prevention

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AAB83358
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29-NOV-1999;
08-MAR-2000;
16-NOV-2000;
                                                                                                                                                                                                 WPI; 200
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This sequence is the NOV2 protein. The invention relates to the NOV1-NOV16 proteins, and their coding sequences. The proteins have Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and
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                                                                           Claim 1; Page 10-13; 141pp; English.
                                                                                                                                                        Novel human polypeptides
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                                                                                                                                      preventing,
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DB; AAF87113.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         produce NOVX proteins, by inserting the nucleic acid into a cell and culturing it to express the protein. The DNA may be used as DNA probes i assays to detect and quantitate the presence of similar DNAs in samples, and which patients may need restorative therapy. The NOVX protein may also be used as antigens in the production of antibodies (Abs) against NOVX and in assays to identify modulators of NOVX expression and activity. The anti-NOVX Abs and antagonist are used to down regulate
                                      serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth nigration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-QT syndrome;
                                                                                                                             NOV; Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception;
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                      cardiovascular
                                                                                                                                                                                                                                                                                                                              AAB83365 standard;
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                      disease;
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hypertrophic cardiomyopathy; v3; NOV4; NOV5; NOV6; NOV7; N
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Вb QΥ 밁 γ

569 VLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSG

628 127 Best Local Similarity

Conservative

37;

Mismatches

16.8%; 75.7%;

Score 1318.5; D Pred. No. 4e-81;

DΒ 39; 22;

Length

1;

Gaps

1;

509

RIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAK 568 qvkdwdkyglmpqvlryhvvachqlllenlklisnatslqgepivisvsqstvyinnkak

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Cytostatic; contraceptive; antinfilammatory; immunomodilatory; and crime of diseases associated with inappropriate NOVX C diagnosis and treatment of diseases associated with inappropriate NOVX C expression. They may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome C that affect the activity of protein by expressing inactive proteins or to supplement the patients own production of protein acid into a cell and C culturing it to express the protein. The DNA may be used as DNA protein may c assays to detect and quantitate the presence of similar DNAs in samples, and which patients may need restorative therapy. The NOVX protein may c activity. The anti-NOVX Abs and antagonist are used to down regulate c presence of NOVX in samples, Disorders that may be used for detecting the cexpression and activity. The anti-NOVX Abs are used to down regulate c presence of NOVX in samples. Disorders that may be prevented, diagnosed and/or treated vary depending on the NOVX protein. NOV1, NOV3, NOV5, NOV9. Il and NOV13-16 have casein kinase II phosphorylation sites c characteristic of serine/threonine kinases, and are used to treat C winase-related disorders (e.g. Peutz-Jeghers syndrome, cellular collection, cell structure and motility and protein management, and are used to treat cused to treat cancers, inflammatory disorders, immune disorders and custoffers and are homologous to EGF-like
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08-MAR-2000;
16-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-648134/74.
N-PSDB; AAF87120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOV11; NOV12;
Sequence
                                  hypertrophic cardiomyopathy, long-QT
                                                                         cellular adhesion disorders. NOV6-10 are homologous to EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 32-33; 141pp; English.
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                                                   proteins and are used to treat cardiovascular disease
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2000US-0715417.
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08-MAR-2000;
16-NOV-2000;
Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NOVX expression. They may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins or to supplement the patients own production of protein. They are used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOV; Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein Kinase II phosphorylation site; contraception; serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-QT syndrome; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOV1; NOV2; NOV3; NOV4; NOV5; NOV6; NOV7; NOV8; NOV9; NOV10;
                                                                                                    This sequence is the NOV7 protein. The invention relates to the NOV1-NOV16 proteins, and their coding sequences. The proteins
                                                                                                                                                    Claim
                                                                                                                                                                                          Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and
                                                                                                                                                                                                                                         N-PSDB;
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une disorders
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DB; AAF87118.
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                                                                                                                                                                                                                                                                                   Vernet C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cc produce NOVX proteins, by inserting the nucleic acid into a cell and cc culturing it to express the protein. The DNA may be used as DNA probes in Cc assays to detect and quantitate the presence of similar DNAs in samples, CC also be used as antigens in the production of antibodies (Abs) against CNOVX and in assays to identify modulators of NOVX expression and cativity. The anti-NOVX Abs and antagonist are used to down regulate expression and activity. The anti-NOVX Abs are used for detecting the presence of NOVX in samples. Disorders that may be prevented, diagnosed CC and/or treated vary depending on the NOVX protein. NOV1, NOV3, NOV5, NOV9-11 and NOV13-16 have casein kinase II phosphorylation sites characteristic of serine/threonine kinases, and are used to treat CC kinase-related disorders (e.g. Peutz-Jeghers syndrome, cellular CC kinase-related disorders (e.g. Peutz-Jeghers syndrome, cellular CC proliferation and contraception). NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (EGF)-like super family and are involved in, e.g. regulation, cell structure and motility and protein management, and are used to treat cancers, inflammatory disorders, immune disorders and are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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  inflammatory disorder; cellular adhesion disorder; lnmune disorder; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOV1; NOV2; NOV3; NOV4; NOV5; NOV6; NOV6; NOV7: NOV8. NOV9.
                                                                         serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth migration; cell structure; motility; cancer; immune disorder;
                                                                                                                                      NOV; Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used to treat cancers, inflammatory disorders, immune disorders and cellular adhesion disorders. NOV6-10 are homologous to EGF-like fibrillin proteins and are used to treat cardiovascular disease e.g. \frac{1}{2}
                                                                                                                                                                                                                                                                                       AAB83359;
                                                                                                                                                                                                                                                                                                                                AAB83359 standard; Protein; 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIOTPRCCHGYFMPDCQACP 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLGGRCDTFTTFDIPGECGSCIFTPKCPLKSKPKGVKKKCIYNPLPFRRNVEGCQNLCTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234;
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                                                                                                                                                                                                                                           (first entry)
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73.1%;
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Pred. No. 1.1
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therapy; nov12;

syndrome;

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                                                                                                                                                                                                                                                                                                       Cytostatic; contraceptive; antinfiammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevention, conditions and treatment of diseases associated with inappropriate NOVX contraceptive; and diseases associated with inappropriate NOVX contraception. They may be used to treat disorders associated with decreased contraception. They may be used to treat disorders associated with decreased contraception. They may be used to to supplement the patients own production of protein. They are used to culturing it to express the protein. The DNA may be used as DNA probes in contraception in the protein. The DNA may be used as DNA probes in contractive protein and quantitate the presence of similar DNAs in samples, continuity. The anti-NOVX and in assays to identify modulators of NOVX expression and contraception and activity. The anti-NOVX abs are used for detecting the presence of NOVX in samples. Disorders that may be prevented, diagnosed contracteristic of serine/threonine kinase II phosphorylation sites characteristic of serine/threonine kinases, and are used to treat contraception. NOV2 protein mov5.

CC NOV7, NOV9-11 and NOV13-16 have casein kinase II phosphorylation sites characteristic of serine/threonine kinases, and are used to treat contraception. NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (EGF)-like super family and are involved in, e.g. regulation of cell development, apoptosis, cell adhesion, growth migration, cell structure and motility and protein management, and are used to treat cancers, inflammatory disorders, immune disorders and cellular contraception. Contraception and are used to treat cancers, inflammatory disorders, immune disorders e.g. broaders and are used to treat cancers, inflammatory and are homologous to EGF-like contracted in treat cancers.
                                                                                                                                                           Matches
                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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16-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAY-2001
                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is the NOV3 protein. The invention relates to the NOV1-NOV16 proteins, and their coding sequences. The proteins have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-NOV-1999;
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                                                                                                                                                                                                                                                                                               hypertrophic cardiomyopathy,
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                                      924
                                                                                               864 LCWHGRFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVH 923
    61
                                                                                                                                                                               Local Similarity
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DB; AAF87114.
atckenntcecnldyegdgitctvvdfckqdnggcakvarcsqkgtkvscscqkgykgdg
                  ATCTENNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDG
                                                                             mcwpgrfgpdclpcgcsdhgqcddgitgsgqclcetgwtgpscdtqavlsavctppcsah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Page 14-17; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders
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                                                                                                                                                                                                                                                             244 AA
                                                                                                                                                             Conservative
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2000US-0715417
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99US-167785P
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84.2%;
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                                                                                                                                                           19;
                                                                                                                                                                             Score 1209; DB 2: Pred. No. 3.7e-74
                                                                                                                                                                                                                                                                                               long-QT syndrome and marfan syndrome
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                                                                                                                                                             Mismatches
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                                                                                                                                                                                                 DB 22;
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                                                                                                                                                                                               Length
                                                                                                                                                           Indels
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RESULT
AAB42164
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 31-MAR-1999;
02-APR-1999;
05-APR-1999;
nucleic vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hyperte neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB42164 standard;
              the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder nucleic acids can be used to express ORFX proteins in gene therapy
                                                                   antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining
                                                                                                                                                                             AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-602362/57.
N-PSDB; AAC76373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vulnerary; antipsoriatic; antiparkinsonian;
anticonvulsant; osteopathic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ORFX ORF1928 polypeptide sequence SEQ ID NO:3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-2001
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                                                                                                                                                                                                                                                        Claim 11;
                                                                                                                                                                                                                                                                                        useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; open
                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and peptides derived from open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mmunostimulant; thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             damage; cartilage damage; antiinflammatory disease;
nbosis; contraceptive.
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 acids can be used to express ORFX proteins. The proteins and nucleic acids may be used
                                                                                                                                                                                                                                                      Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reading frame; ORFX; detection;
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99US-0127728
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Best Local Similarity
Matches 217; Conserv
19-NOV-1999;
29-NOV-1999;
08-MAR-2000;
16-NOV-2000;
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CC produce Novx proteins, by inserting the nucleic acid into a cell and CC culturing it to express the protein. The DNA may be used as DNA probes in CC assays to detect and quantitate the presence of similar DNAs in samples, CC and which patients may need restorative therapy. The NOVX protein may CC also be used as antigens in the production of antibodies (Abs) against CC NOVX and in assays to identify modulators of NOVX expression and CC activity. The anti-NOVX Abs and antagonist are used to down regulate CC expression and activity. The anti-NOVX Abs are used for detecting the CC presence of NOVX in samples. Disorders that may be prevented, diagnosed CC and/or treated vary depending on the NOVX protein. NOV1, NOV3, NOV5, CC (NOV7, NOV9-11 and NOV13-16 have casein kinase II phosphorylation sites CC characteristic of sering/threonine kinases, and are used to treat CC kinase-related disorders (e.g. Peutz-Jeghers syndrome, cellular CC the epidermal growth factor (REF)-like super family and are involved in, CC e.g. regulation of cell development, apoptosis, cell adhesion, growth CC used to treat cancers, inflammatory disorders, immune disorders and are CC used to treat cancers, inflammatory disorders, immune disorders and collinar adhesion disorders NOV6-10 are homologous to FEF-11ke.
                                           cellular adhesion disorders. NOV6-10 are homologous to EGF-like fibrillin proteins and are used to treat cardiovascular disease hypertrophic cardiomyopathy, long-QT syndrome and marfan syndrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression by rectifying mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins of supplement the patients own production of protein. They are used to
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis and treatment of diseases associated with inappropriate NOVX expression. They may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiovascular activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human polypeptides an for preventing, diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is the NOV10 protein. The invention relates to the NOV1-NOV16 proteins, and their coding sequences. The proteins have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 35; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lichenstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences may be used in the prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nd the nucleic and treating (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vernet C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   c acids that encode them useful e.g. cancer, inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fernandes
                                                marfan syndrome
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                                                                                                                                                                                                             VLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSG
                                                                                                                                                                                                                                           RIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAK 568
                         TLGGRCDTFTTFD
                                                                            DLPRSASWKTLQGSELSVRCGTGSD1GELFLNEQMCRF1HRGLLFDVGVAYG1DCLLMNP
                                                                                                      {\tt llsvitdpihtpvtlfwptdqalhalpaeqqdflfnqdnkdklkeylkfhvirdakvlav}
                                                                                                                                  LLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALAS
                                                                                                                                                           iis s diisting iv hiid kllspknllit pkdnsgril qnlttlatnngyik fsnliqdsg
                                                                                                                                                                                                                                                                      al Similarity
197; Conserv
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                                                                                                                                                                                                                                                                                 13.68;
77.98;
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                                                                                                                                                                                                                                                                                 Score 1067;
Pred. No. 2
                                                                                                                                                                                                                                                                    Mismatches
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RESULT 11
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Matches 162
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                                                                                                                                                                       The present sequence represents a hyaluronan-binding protein. The specification describes four hyaluronan-binding protein, known as WF-HABP, WF-HABP, OE-HABP, and BM-HABP. The polypeptides are useful for treating diseases such as proliferative conditions, metastas, inflammation, ischemia, host defence dysfunction, immune surveillance
                                                                                                                                                                                                                                                                New hyaluronan-binding proteins, known as full-length WF-HABP, WF-OE-HABP and BM-HABP, useful for treating proliferative conditions, metastasis, inflammation, ischemia, arthritis and multiple scleros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A human hyaluronan-binding protein,
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                                                                                                                                                                                                                                           Claim 11; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hyaluronan-binding protein WF-HABP; OE-HABP; BM-HABP;
 1030
                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                 Hastings
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME
(AMNA-) AMERICAN NAT
                                                                                                                                                dysfunction and allergy.
                                            971
                                                                                                                                                             dysfunction, arthritis,
                                                                  Local Similarity 40.1 nes 162; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     defence dysfunction; immune surveillance dysfunction; iple sclerosis; autoimmunity; immune dysfunction; alle
EPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEA 1089
                                  VSCSCKKGYKGDGYSCIEIDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDC- 1029
                                                                                                                                                                                                                                                                                                               2000-452376/39.
)B; AAA57363.
                    vtctclpdyegdgwscrarnpctdghrggcsehanclstglntrrcechagyvgdglqcl
                                                                                                                                                                                                                                                                                                                                                 GA,
                                                                                                                           457 AA;
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358
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                                                                              9.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "link domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "unspecified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "EGF-like type 2 domain"
                                                                                                                                                                                                                                                                                                                                                   Tsifrina
                                                                                                                                                            multiple sclerosis,
                                                                56;
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                                                                              Score 774; DB 2 Pred. No. 3e-44;
                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid encoded by TNT'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation;
                                                                                         DB 21;
                                                                    170;
                                                                                                                                                             autoimmunity,
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                                                                                       Length 457;
                                                                    Indels
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                                                                    12;
                                                                                                                                                                                                                                                                   sclerosis
                                                                                                                                                                                                                                                                                          WF-HABP,
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RESULT 1
AAR05222
It is encoded by an open reading frame contained within the sequence of clone 533 which was derived from an E. tenella genomic library screened with radioactively labelled cDNA encoding the GX5401 antigen. It is of about 250 Kd. It carries several repeated peptide sequences and is rich in cysteine residues. The open reading frame also encodes a potential signal sequence for protein secretion. Also new are an expression vector contg. cloned gene, and host cells transformed with the vector. The transformed cells are used in a vaccine to immunise birds against avian coccidiosis. By labelling the peptides, they can be used as a type-specific probe. May also be used in an assay to detect a bagainst the coccidia. The Abs are used to identify transformed cells
                                                                                                                                                                                                                                                                                 Cloned gene or fragment encoding antigenic protein which binds with antibodies against avian coccidia. transformed cells used in vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1320
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                                                                                                                                                                                                                                                   Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                      Anderson DM,
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DB; AAQ03324.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WDVFCYRMKDVNCTCKAGYVGDGFS-CSGNLLQVLMSFPSLTNFLTEVLAFSKSSARGQA 1208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; protein;
                                                                                                                                                                                                                                                   Page 93; Fig 14; 134pp; English
                                  DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CORP
                                                                                                                                                                                                                                                                                                                                                                                                      McCandliss
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cc polypeptide (II) sequences. (I) is useful as hybridisation probes, cc polymerase chain reaction (PCR) primers, oligomers, and for chromosome. cc and gene mapping, and in recombinant production of (II). The cc polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques ct or restore normal activity of (II) or to treat disease states involving cc (II). (II) is useful for generating antibodies against it, detecting or cc quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical cmaging of sites expressing (II). (I) and (II) are useful for treating cc disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cc amino acid sequences. ABG00010-ABG30377 represent novel human
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                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID No 36761; 103pp; English
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23-AUG-2000;
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food supplement; medical imaging; diagnostic; genetic (
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RSCSEHGQCDEGITGSGECLCETGWTAA --
                             cmimnggcdtqctn---segsy----ecscsegyalmpdgrscadidec-
                                                                                                                                                ececfegyesgfmmmkncmdidgcernpllcrggtcvntegsf---
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                                                        GGPDTPCNNRGMCRDLYTPMGQCLCHTGF----NGTAC---ELCWHGRFGPDCQP
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capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB5737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from

The invention relates to an isolated nucleic acid detection reagent

invention

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-VHGRCSQGPL-GDGSCDCDVGWRGVKCDMEITTDNCN--GTCHTSANCLLDPDGKASC
                                                                                                                                                                                                                                                                                                                                      scqc--mpgytgqkcetniddcvtnpcgnggtcidkvngykcvckvpftgrdceskmdpc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qkqi-necesnpcqfdghcqdrvgsyycqcq----ag-----tsgkncevnv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLEINPCLENHGGC-DR--------NAECTQTGP--NQAVCN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KCAAGFRGNGTVC-TAINACETSNGGCSTKADCKRTTPGNRVCVCKAGYTG-----DGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chadaicdtspingsyacscatgykgvdcsedi--decdggspcehngicvntp-gsyrc
                                                                                                   dgingy-ncsclagysgancgyk---lnkcdsnpclngatcheqnneytchcpsgftgk-
                                                                                                                                                           khcetdineclsqpcqngatcsqyvnsytctcplgfsgincqtndedctessclnggsci
                                                                                                                                                                                         TACEL-----CWHGRF-----
                                                                                                                                                                                                                        cl----
                                                                                                                                                                                                                                                CTVVIQTPRCCHGYFMPDC----QACPGGPDTPCNNRGMCRDLYTPMG--QCLCHTGFNG
                                                                                                                                                                                                                                                                             asnrckneakctpssnfldfsctcklgytgrycdedidecslsspcrngasclnvpgsyr
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                                         -qcseyvdwcgqs--pcengatcsqmkhqfsckcsagwtgk--lcdvqtiscqdaadrkg
                                                                                                                                EGITGSGECLCETGWTAASCDTPTAVFAVC-TPACSVHATCTENN---TCVCNLNYEGDG
                                                                      ITCT-VVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSC-IEIDPCADGV----
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NGGCHEHATCRMTGPGKHKCECKSHYVGDGVDCEPEQLPLDRCLQDNGQCHP
                                                                                                                                                                                                                   -ctkgyegrdcaintddc---asfpcqnggtcld---gigdysclcvdgfdg
                                                                                                                                                                                                                                                                                                             KCI--YNPLPFR-----
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23.1%;
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Pred. No. 1.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ngykcecprgfydahclsdvdeca
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20 Вb

131 EIQKNRCDNNDT------IIVRGECGK-CSQQAPCPLETKPLRETRKCIYSIYFMG 179

279

qlqpnachnggtcfntlgghscvcvngwtgescsqnid----

-dcatavcfhg

Query Match Best Local S Matches 272

Local Similarity

Conservative

6.0%;

Score 469; DB Pred. No. 1.4e 11; Mismatches

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Length 2321; Indels

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Gaps

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RESULT 1
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                       This sequence represents the human Notch3 protein, a transmembrane receptor protein involved in lateral inhibition and regulating developmental cascades of neurogenic genes. Mutated Notch3 proteins are thought to be involved in neurological disorders, especially of the cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL) type. Blocking expression of a mutated Notch3 gene or by substitution therapy with non-mutated Notch3 gene or by substitution treat CADASIL or related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Notch3; transmembrane receptor; lateral inhibition; required developmental cascade; neurogenic gene; mutant; neurological discrebial autosomal dominant arteriopathy; subcortical infarct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW49698 standard;
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                                                                                                                                                         Claim 2;
                                                                                                                                                                                                  Human Notch3 nucleic acids - and methods for identifying pre-disposition to cerebral autosomal dominant arteriopathy
                                                                                                                                                                                                                                            N-PSDB; AAV57001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Notch3 protein
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Sequence
                                                                                                                                                                                     sub-cortical infarcts
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                                                                                                                                                                                                                                                                                        Bach
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                                                                                                                                                         Fig 1.1-1.8;
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2321 AA;
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Db

1148	YHLCSAG-WLESGRVAYPTTYASQKCGANVVGIVDYGSRANKSE	1106
1163	cqhggscidlvarylcscppgtlgvlceinedd	1131
1105	CHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIAT	1046
1130		1079
1045	GCHEHATCRMTGPGKHKCECKSHYVGDGVDCEPEQI	999
1078	:: yclcppgwsgrl	1021
998	QVSCSCKKGYKG	970
1020	<pre>vcsaahpgfrctclesftgpqcqtlvdwcsrqpc</pre>	976
969	VCTPA-CSVHATCTENNTCVCNLNYEGDGITC-TVVDFCKQNNGGCAKVA	915
975		922
914	WEANTLOULT	0 0
862 921	GMCRDQCLCHTGFNGTAC	839
861	qqdvdecagpapcgphgictnlagsfsctchggytgpscdqdlndcdpnpclng	808
838	YNPLPERRNVEGCQNLCTVVIQTPRC-CH-GYFMPDCQACPGGPD-TPCNNR	790
807	-vggrqcellspctpnpcehggrcesapgqlpvcscpggwggprc-	764
789	IFT	737
763	ardacesqpcraggtcssdgmgfhctcppg	734
736	FHVIRDSKALASDLPRSASWKTLOGSELSVRCGTGSDIGELFLNEOMCRFIHRGLLFDVG	677
733	icydapggfrcvcepgwsgprcsqsl	708
676	SVITDSIH	619
707	;	670
618	TTVAANHGYT	563
669		622
562	HVVGCQQLLLDNLKVTTSATTLQG	511
621	ytgtr-cesqv-decrsqpcrhggkcldlvdkylcrcpsgttgvncevni	574
510	TRACHTACAST TAVALLA CONTRACTOR TO THE ACCURACY OF THE PROPERTY	л . Э
573	dq-pdqvecrcaeqfeqtlcdrnvddcspdp-chhurcvdqiasfscacapq	524
451))
395 523	<pre>ETSNGGCSTKADCKRTTPGNRVCVCKAGYTGDGIVC-LEINPCLENHGGCDRNAECT :: </pre>	340 474
4/3		419
339	CDVGWRGVKCDMEITTDNC-NGTCHTSANCLLDPDGKASCKCAAGFRGNGTVCTA-INAC	282
418	vdecsiganpcehlgrcvntqgsflcq	370
281	GVNGTGTCQCGLGFNGTACETCTEGKYGIHCDQACSCVH-GRCSQGPLGDGSCD	229
369	atchdrvasfycacpmgktgllchlddacvsnpchedaicdtn	327
228	WD	180

В Qy

В Qy Qy

9

Db

Qy Дb DЬ Qy В Qy В VO DЬ Qy Ър Qy DЪ 04 Дδ Qy В Qy ОУ

Db	Оy	Db
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Search completed: June 17, 2002, 12:30:21 Job time: 252 sec

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MGD; MGI:95490; Fbn2.

InterPro; IPR000152; Asx_hydroxyl.

InterPro; IPR001581; EGF-like.

InterPro; IPR001881; EGF-Ca.

InterPro; IPR001881; EGF_CI.

InterPro; IPR0012212; Tnf-C2H2.

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           Maslen C.L., Corson G.M., Maddox B.
"Partial sequence of a candidate generative 352:334-337(1991).
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01-JUN-1994
16-OCT-2001
                                                                                                                                                                    Hum. Mol. [2]
SEQUENCE
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SEQUENCE
        SEQUENCE OF 813-1313 FROM
                                                                                                      multidomain
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                                                                                                                          Corson G.M., Chalberg S.C., Dietz H.C "Fibrillin binds calcium and is coded
                                                                                                                                               SEQUENCE OF 1-932 FROM N.A. TISSUE=Placenta, and Fibroblast; MEDLINE=94010947; PubMed=7691719;
                                                                                                                                                                                                   defective
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Pangilinan T., Bonadio J
"Genomic organization of
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                  "Fibrillin-1 mutations in
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J. Mo
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"Solution structure of the transforming growth factor protein-like module, a domain associated with matrix f EMBO J. 16:6659-6666(1997).
                                          MEDLINE=93250834;
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MEDLINE=91304569; Pul
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Collod-Beroud G., Beroud C., Ades
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Knott V., Downing A.K., Cardy C.M.
"Calcium binding properties of an
pair from human fibrillin-1.";
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  fibrillin gene.";
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85:597-605(1996).
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age of Marfan syndrome a
different fibrillin genes
e 352:330-334(1991).
                              н.с.,
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                                                                                                                                          =91304569; PubMed=1852208;
.C., Cutting G.R., Pyeritz R.E.,
G.M., Puffenberger E.G., Hamosh
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Saraiva J.M., Pyeritz R.E., (
of fibrillin (FBN1) missense
cysteine residues in EGF-like
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F., Hollister D.W.;
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MEDLINE=94108431;
Tynan K., Comeau F
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Hewett D.R., Lynch J.R., Smith R., Sykes B.C.;
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disrupt calcium binding of the epidermal growth factor-li
Hum. Mol. Genet. 2:475-477(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                  syndrome
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                                                                                                                                  VARIANT MFS CYS-122
MEDLINE=94314977; Pu
                                                                                                                                                                                            MEDLINE=94272487; PubMed=8004112; Hayward C., Rae A.L., Porteous M.E. "Two novel mutations and a neutral
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                                             MEDLINE=94351682;
                                                                                    variant
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                                                                                                                Saxne T.,
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                                                                             ne T., Tornqvist K., Peltonen L.;
extra cysteine in one of the non-calcitor-like motifs of the FBN1 polypeptide iant of Marfan syndrome.":
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ation screening of complete fibrillin-1
ive new mutations, including two in 8-c;
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                           D.R., Lyr
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19:573-576(1994).
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                           Lynch J.R., se mutation
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Child A., Kainulain
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970; PubMed=7977366;
Raghunath M., Loenng
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         31:338-339(1994)
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94:709-713(1994).
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                           PubMed=8071963;
h J.R., Child A., Sykes
utation of fibrillin in
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"A novel mutation in the fibrillin gene (FBN1)
arachnodactyly.";
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K-2447 AND R-2511.
MEDLINE=94184368; PubMed=8136837;
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MEDLINE-95174777; PubMed=7870075;
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01-FEB-1996
16-OCT-2001
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             VARIANTS CCA HIS-1.1.14.
MEDLINE=98407789; PubMed=9737771;
                                                   Purnam E.A., Zhang H., Ramirez F., Milewicz D.M.; "Fibrillin-2 (FBN2) mutations result in the Marfan-like disorder, congenital contractural arachnodactyly."; Nat. Genet. 11:456-458(1995).
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                                                                                                                                  "Linkage of Marfan syndrome and two different fibrillin genes."; Nature 352:330-334(1991).
                                                                                                                                                                                   MEDLINE-91304567; PubMed-1852206;
Lee B., Godfrey M., Vitale E., Hori H.,
Tsipouras P., Ramirez F., Hollister D.;
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                               Fibrillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FBN2_HUMAN P35556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1483
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                                                                                                                                                                                                                            SEQUENCE OF 752-1505 FROM N.A
                                                                                                                                                                                                                                                                                                                     MEDLINE=94165150; PubMed=8120105;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLCKEGYTGDGFTCTDLDECSENLNLCGNGQC-----LNAPGGYRCECDMGFVPSADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSCKKGYKGDGYSCIEIDPCADGV----NGGCHEHATCRMTGPGKHKCECKSHYV--GDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNCMDIDECQRDPLLCRGGVCHNTEGSYRCECPPGHQLSPNISACIDINECELSAHLCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VDCEPEQLPLDRCLQDN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HNCGKHAVCT--NTAGSFKCSCSPGWIGDGIKCTDLDECSNGTHMCSQHADCKNTMGSYR 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PACSVHATCTENNT-----CVCNLNYEGDGTTCTVVDFCKQNNGGCAKVAKCSQKGTQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---DMKTCVDVNECDLNPNICLSGTCENTKGSFICHCDMGYSGKKGKTGCTDINECEIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDCQPRSCSEHGQCD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRCVNLIGKYQCACNPGYHSTPDRLFCVDIDECSIMNGGCETFCTNSEGSYECSCQPGFA 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----IDCLLMNPTL--GG-----RCDTFTTFDIPGECGSCIFTPKCPLKSK--PK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMPDQRSCTD1DECEDNPNICDG-GQCTNIPGEY----RCLCYDGFMASE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MPDCQACPG---GPDTP--CNNRGMCRDL---YTPMGQCLCHTGFNGTACELCWHGRFG
 D.,
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                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --VKKKCIYNP----LP---FRRNVE
                                                                                                                                                                                                                                                                                                                                                                                        Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel.
(Rel.
(Rel.
Gasner C.,
                                                                                                                                                                                                                                                                                                                                                                                                                               precursor
                                                                                                                                                                                                                                                                                                                                                                                                    (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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 Francke U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GOCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAK 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             annotation
                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -EGITGSGECLCETGWTAASCDTPTAVFAVC---T
                                                                                                                                                                        a phenotypically related
 Maslen
                                                                                                                      AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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                                                                                                                    VARIANT
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                                                                                                                                                                                                                                                                                                                                                                           Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GCQNLCTVVIQTPRC-CHGYF-
                                                                                                                                                                                                                                                                     matrices
                                                                                                                                                                                                                                                                                novel microfibrillar
                                                                                                                                                                                                                                                                                                          Sanguineti
                                                                                                                                                                                                 M.-G.,
                                                                                                                      ILE:
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                                                                                                                                                                                                   Sarfarazi
                                                                                                                                                                         disorder to
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InterPro: IPR002212; TB.
Pfam; PF00008; EGF; 45.
Pfam; PF000683; TB; 9.
Pram; PF00683; TB; 9.
PRINTS; PR00010; EGF_CA; 43.
SMARF; SM00017; EGF_Like;
PROSITE; PS00010; ASX_HYDR
PROSITE; PS00022; EGF_L; 2.
PROSITE; PS01186; EGF_CA;
PROSITE; PS01187; EGF_CA;
EXYLTACCHILLIAT MALLIX; COLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arachnodactyly.";

Am. J. Med. Genet. 92:7-12(2000).

Am. J. Med. Genet. 92:7-12(2000).

FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS THAT BINDS CALCIUM. FIBRILLIN-2-CONTAINING MICROFIBRILS REGULATE THE EARLY PROCESS OF ELASTIC FIBER ASSEMBLY.

I-DISEASE: DEFECTS IN FBN2 ARE THE CAUSE OF CONGENITAL CONTRACTURAL ARACHNODACTYLY (CCA) (ALSO KNOWN AS BEALS SYNDROWE). CCA IS PHENOTYPICALLY SIMILAR TO MARFAN SYNDROME, BUT DOES NOT EFFECT TH AORTA AND THE EYES.

I-SIMILARITY: CONTAINS 43 CALCIUM-BINDING AND 4 NON-CALCIUM BINDING EGF-LIKE DOMAINS.

I-SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Belleh S
Godfrey
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InterPro;
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entities
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between
the Euro
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MEDLINE-20259236; PubMed=10797416;
Belleh S., Zhou G., Wang M., Der Ka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A single mutation that results in an asp-to-his substitution partial exon skipping in a family with congenital contractual arachnodactyly."

Hum. Genet. 103:22-28(1998).
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EMBL; X62009; -; NOT_AN
PIR; S17063; S17063.
PIR; S31101; S31101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Godfrey M.;
"Two novel fibrillin-2 mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P35555;
MIM; 121050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            IS; PRO0010; EGFBLOOD.

I; SM00179; EGF_CA; 43:

I; SM00017; EGF_Like; 3

I; SM00001; ASX_HYDRO

ITE; PS00022; EGF_1; 2.

ITE; PS01186; EGF_2; 37:

ITE; PS01187; EGF_CA; 4

ITE; PS011A1 matrix; Calci

Lt; Signal; Multigene f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000152; ASX_hydroxyl.
IPR000561; EGF-like.
IPR001881; EGF_Ca.
IPR001438; EGF_II.
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$31101.
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; EGF_CA; 43.
; EGF_like; 3.
10; ASX_HYDROXYL;
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 Wang M., Der Kaloustian
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POTENTIAL.

FIBRILIN

EGF-LIKE 1

EGF-LIKE 2

EGF-LIKE 4

FIGF-LIKE 5

FIGFBP 1.

EGF-LIKE 6

EGF-LIKE 7

EGF-LIKE 9

EGF-LIKE 9

EGF-LIKE 9

EGF-LIKE 1

EGF-LIKE 1
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                                                                                                                                                                                                                                                                                                                                              ng; Glycoprotein;
isease mutation; I
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E 2, NON-CALCIUM BINDING.
E 3, NON-CALCIUM BINDING.
E 4, CALCIUM-BINDING.
E 5, CALCIUM-BINDING.
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Polymorphism.
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                                                                                    CAVGAAWGTECEECPKPGTKEYETLCPRGAGF---ANRGDVLTGRPFYKDINECKAFPGM
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                                                               LPRSASWKTLQGSELSVRCGTG-----
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7; Mismatches 400;
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MEDLINE=90385285; PubMed=2402639;
Coffman C., Harris W., Kintner C.;
"Xotch, the Xenopus homolog of Drosophila Science 249:1438-1441(1990).
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01-MAY-1991
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                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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NCBI_TaxID=8355;
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                                                                       ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a by non-profit institutions as long as
                                                                                                                                               SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS. SIMILARITY: CONTAINS 4 LIN/NOTCH REPEATS.
                                                                                                                                                                                                           mitted (JUN-1996) to the EMBL/GenBank/DDBJ databases SUBCELLULAR LOCATION: Type I membrane protein. DEVELOPMENTAL STAGE: EXPRESSED ALMOST UNIFORMLY IN 1
                                                                                                                     SWISS-PROT entry is copyright. It is produced through a
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Metazoa; Chordata; Crania
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(Rel. 34, Last sequence up
(Rel. 40, Last annotation
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EMBL; M33874;

AAB02039.1;

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Interpro; iPROUZID; ANK.
Interpro; iPROUZID; ANK.
Interpro; iPROUZIS; ASX_hydroxyl.
Interpro; iPROUZIS; ESF_1ke.
Interpro; iPROUZIS; ESF_2.
Interpro; iPROUZIS; ESF_CA:
Interpro; iPROUZIS; ESF_LA:
Interpro; iPROUZIS; ESF_CA:
Interpro; iPROUZIS; ESF_LA:
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  GVNGYKCDCEAGW-
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                                                                                                                                                                                                                                                                                     TG
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                       PVTVF-----
                                           NPCRNGGTCKDQI
                                                                                    TCPKGTTGVNCETKIDDCASNLCDNGKCIDKIDGYECTCEPGYTGKLC---NININECDS
                                                                                                         SVSQDTVFINNEAKV--LSSDIISTNGVIHVID----
                                                                                                                               NECIPDPCHYGTCKDGIATFTCLCRPGYTGRLCDNDINECLSKPCLNGGQCTDRENGYIC
                                                                                                                                                   EPRIKDWDQQGLMSQVLRYHVVGCQ~~~~QLLLDNLKVTTSATTLQGEPVS~~~~I
                                                                                                                                                                        KINEFRCDCPTGFSGNLCQHDFDECTSTPCKNGAKCLDGPNSYTCQCTEGFTGRHCEQDI
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                                                                                                                                                                                                                                                             \texttt{TGPACNNDVDECSLGANPC--EHGG-----RCTNTLGSFQ--CNCPQGYAGPR--CEIDV}
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                                                              TPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITD----
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                   WPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPR
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1; Mismatches
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Pred. No. 4.4e-26;
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  SGSNCD--
                                                                                                                                                                                               ---LAGPGPFTVFAPLSSSFNH----
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                                          HDHMCLSEVNECNSNPCIHGACHD
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INNNECESNPCMN
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NOTC_DROME
P07207; P0411
01-NOV-1986
01-MAR-2002
ALKALN=Canton-S, and Oregon-R; TISSUE=Embryo; MEDLINE=87064624; PubMed=3097517; Kidd S., Kelley M.R., Young M.W.; "Sequence of the notch locus of Drosophila melanogaster: of the encoded protein to mammalian clotting and growth f Mol. Cell. Biol. 6:3094-3108(1986).
                                                                                                                                                                    SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-Oregon R; TISSUE=Embryo;
MEDLINE=66079539; PubMed=9935325;
Wharton K.A., Johansen K.M., Xu T., Artavanis-T
"Nucleotide sequence from the neurogenic locus
"Nucleotide sequence from the neurogenic locus
                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1986 (Rel. 03, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Neurogenic locus Notch protein precursor.
N OR EG:140G11.1 OR EG:163A10.2 OR CG3936.
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Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
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                                                                                                                                              43:567-581(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGSRANKSEMWDVF-----CY-----RMKDVNCTCKAGYVGDGFSCSGNLLQVL
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RA Yell S.
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Science 287:2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wharton
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PubMed=2981631;
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ions at the Notch locus of Drosophila
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EMBL; AL035436; CAB37610.1; -.
EMBL; AL035395; CAB37610.1; JOINED.
EMBL; M12175; AAA74496.1; -.
EMBL; M16025; AAA28726.1; -.
PIR; A24720; A24768.
PIR; A24768; A24768.
PIR; A24768; A34768.
PIR; A24768; A34768.
                                                                                                                                                                                                                                                                                InterPro; IPR002110; ANK.
InterPro; IPR000152; Asx_hydro
InterPro; IPR000551; BGF-11ke.
InterPro; IPR000742; BGF_2.
InterPro; IPR001881; BGF_Ca.
InterPro; IPR001881; BGF_II.
InterPro; IPR000800; Notch.
                                                                                                                               PROSITE;
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 DOMAIN
DOMAIN
                                 DOMAIN
TRANSMEM
                                                                                                                                                                           PRINTS; PR01452; NOTCH.
SMART; SM002748; AK; 4.
SMART; SM000179; EGF_CA; 23
SMART; SM00001; EGF_11ke;
SMART; SM00004; NL; 2.
                                                                                                                                                                                                                                             Pfam; PF00023; ank; 6. Pfam; PF00008; EGF; 36. Pfam; PF00066; notch; 3
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Many cell types specified by Notch function.";
Curr. Biol. 1:120-122(1991).
-i- FUNCTION: NOTCH PROTEIN IS ESSENTIAL FOR PROPER DIFFERENTIATION
                                                          CHAIN
                                                                                                                                                                                                                                     PRINTS; PR00010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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                         DOMAIN
                                                                       SIGNAL
                                                                                            Differentiation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECTODERM.
SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLANEOUS: SEPARATION OF NEUROBLASTS FROM THE E
THE INNER PART OF EMBRYO IS ONE OF THE FIRST STEPS
THE INNER PART OF THE PROCESS IS UNDER CONTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEUROGENIC GENES.
SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
SIMILARITY: CONTAINS 6 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M16152; AAB59220.1;
M16153; AAB59220.1;
M16149; AAB59220.1;
M16150; AAB59220.1;
M16151; AAB59220.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K035U8; AAA28725.1; M13689; AAA28725.1;
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                                                                                                     PS00010; ASX_HYDROXYL;
PS00022; EGF_1; 34.
PS01186; EGF_2; 28.
PS01187; EGF_CA; 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                     PS50088; ANK_REPEAT; 5. PS50297; ANK_REP_REGION;
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                                                                              Signal;
                                                                                                                                                                                                                                     EGFBLOOD
                                                                                          Neurogenesis; Repeat;
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EGF-like.
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CYTOPLASMIC EGF-LIKE 1. EGF-LIKE 2.
                                 EXTRACELLULAR POTENTIAL.
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strictions on its
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SCQC-
                GIDCLLMNPTLGGRCDTFTTFDIPGEC---GSCI----
                                                                                    GLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALA
                                                                                                               SSDIISTNGVIHVIDKLLSPKNLLI----TPKDALGRVLQNLTTVAANHGYTKFSKLIQDS
                                                                                                                                                                        QKQI-NECESNPCQFDGHCQDRVGSYYCQCQ---
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                                                 SDLPRSASWKTLQG-SELSVRCGTG
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                                                                                                                                                                                                                                                                                                                                                                                      269;
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-MPGYTGQKCETNIDDCVTNPCGNGGTCIDKVNGYKCVCKVPFTGRDCESKMDPC
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23.1%;
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Pred. No. 6.7e
97; Mismatches
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Mammalia; |
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Genomics 56:70-77(1999)
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Biery N.J., Eldadah Z.A., Moore C.
                                                                                                                                                                                                                                                                                                                                                                Fibrillin
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                                                                                                               FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICH THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.

PIM: FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH OTHER FORMS INTERMOLECULAR DISULFIDE BONDS OF THE
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                                                               SIMILARITY: CONTAINS
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a; Metazoa;
Eutheria;
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1 (Rel. 40, Last sequent (Rel. 40, Last anno precursor.
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annotation update)
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HSSP; P35555; LAPJ;
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR0001881; EGF_Ca.
InterPro; IPR0001881; EGF_Ca.
InterPro; IPR0001881; EGF_Ca.
InterPro; IPR0001881; EGF_Ca.
InterPro; IPR0001881; EGF_LIX.
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EGEF-LIKE 1

EGEF-LIKE 2

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                                                                           ----ETCFLRYEDEECTLPVVGRHRMDACCCSVGAAWGTEECEECPPRNTPEYEELCPRG
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                                                                                                         SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS. SIMILARITY: CONTAINS 3 ANK REPEATS.
                                                                                                                                                                    SUBCELLULAR LOCATION: Type I membrane TISSUE SPECIFICITY: IN FETAL TISSUES MERAIN STEM AND LUNG. ALSO PRESENT IN METAL STEM AND LUNG. ALSO PRESENT IN METAL STEM AND LUNG. ALSO PRESENT IN METAL STEMPHOLO TISSUES.
                                                                                                                                                                                                                               FUNCTION: MAY BE IMPORTANT FOR NORMAL LYMPHOCYTE F ALTERED FORM, MAY CONTRIBUTE TO TRANSFORMATION OR IN SOME T-CELL NEOPLASMS.
                                               European Bioinformatics Institute.
                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                           the human homolog of the Drosophila notch gene,
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               non-profit and this st
and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
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. 40, Last annotation update)
notch protein homolog 1 precursor
protein TAN-1) (Fragment).
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RT; SM00248; ANK; 5.
RT; SM00179; EGF_CA; 22.
RT; SM00011; EGF_Like; 13.
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 Neurogenesis; Repeat; ignal; Glycoprotein.
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ANK_REP REGION; 1

ASX_HVDROXYL; 20.

EGF_1; 34.

EGF_2; 26.

EGF_CA; 18.
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EGF-like.
EGF_2.
EGF_Ca.
Notch.
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CYTOPLASMIC
EGF-LIKE 2.
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                    DIPGEC ---
                                                                                                      QQDFLFNQDNKDKLKSYLKFHV-
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Pred. No. 7.5e
20; Mismatches
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                                                                                                                                                      microfibrils including the molecular cloning of MAGP-2 (
J. Biol. Chem. 271:1096-1103(1996).
-:- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE
THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBR
LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
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"Sequence of the coding region of
localization to bovine chromosome
Genomics 23:480-485(1994).
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SIMILARITY: C
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                                           EGF-LIKE DOMAINS
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EMBL; L28748; AAA74122.1; -.
HSSP; p35555; IAPJ
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000161; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EGF_II.
InterPro; IPR001212; TB.
Pfam; PF00008; EGF; 46.
Pfam; PF00008; EGF; 46.
Pfam; PF000010; EGFBLOOD.
SMART; SM0010; EGF_Like; 4.
PROSITE; PS00010; ASX_HYDRCXYL; 43.
PROSITE; PS001186; EGF_1; 2.
PROSITE; PS01186; EGF_2; 38.
PROSITE; PS01187; EGF_CA; 45.
Extracellular matrix; Calcium-binding; G1.
Repeat; Signal; Multicepe family.
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CHAIN
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TGFFBP 7.
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TGFFBP 7.
EGF-LIKE 41, C.
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 AW - - NKPCEQCP -
                    FWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSE 703
                                            MRRSLCYRNYYADNQTCDGELLFNMTKKMCCCSYN
                                                                                                                                        RPNPITVI-
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                                                                                                                                                                                                                                                                                                      --LPKYTGDGKV---
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                                                                                                                                                                                                                                                                                                                                                 KADCKRTTPGNRVCVCKAGYTGDGIVCLEINPCLENHGGCDRNAECTQTGPNQAVCNC--
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                                                                                        QCRCPTGYYLNEDTRVCDDVNECETPGICGPGTCYNTVGNYTCICPPDYMQVNGGNNCMD
                                                                                                                QGE-PVSISVSQDTVF
                                                                                                                                                                                     DTACSNEIGVGVSKASCCCSLGKAWGTPCELCPPVNTSEY-
                                                                                                                                                                                                                                  LDPTTCISGNCVNTPGSYT - - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276;
                                                                  KLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITDSIHTPVTV 643
                                                                                                                                                             PFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQL--LLDNLKVTTSATTL
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                                                                                                                                       -LEDIDE--
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Pred. No. 1
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.2e-25;
                                                                                                               INNEAKVLSSDIISTNGVIHVID
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                                                                                                                                       -CQELPGLCQGGKCINTFGSF
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IPSTDEFATLCGSQ
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                  Mech.
                                                                                                                                                                                                                      Bierkamp C., Campos-Ortega J.A.;
"A zebrafish homologue of the Drosophila neurogenic
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebstata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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                                                                                                                         pattern of transcription during early embryogenesis.";
h. Dev. 43:87-100(1993).
FUNCTION: IMPLICATED IN CELL FATE SPECIFICATIONS DURING EMERYO DEVELOPMENT. MAY BE INVOLVED IN THE FORMATION OF NEURAL PLATE, NOTOCHORD AND BRAIN VESICLES.
             SUBCELLULAR LOCATION: Type I membrane protein.

DEVELOPMENTAL STAGE: EXPRESSED IN ALL CELLS IN PREGASTRULATION

STAGES. DURING GASTRULATION IS DIFFERENTIALLY EXPRESSED,

ACCUMULATING PREDOMINANTLY IN THE PRECHORDAL MESODERM AND

NOTOCHORD. AT THE END OF GASTRULATION, EXPRESSED ALONG THE

ANTERIOR-POSTERIOR AXIS INCLUDING THE DEVELOPING NEURAL PLATE
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DIFFERENTIATING MESODERM. ALSO PRESENT IN THE DEVELOPING
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PRINTS; PRO1452; NO
SMART; SM00248; ANN
SMART; SM00179; EGI
SMART; SM00001; EGI
SMART; SM00001; NL,
PROSITE; PS500088;
PROSITE; PS500297;
PROSITE; PS00010; I
PROSITE; PS00010; I
PROSITE; PS001186; I
PROSITE; PS01186; I
PROSITE; PS01187; I
D1fferentiation; NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified entities or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PR
between the
the European
 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BRAIN AND HEAD REGIONS.
SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE F
SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
SIMILARITY: CONTAINS 6 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation—pean Bioinformatics Institute. There are no restrictions on its non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; EGF_CA;
1; Neurogenesis; kep.
1; neurogenesis; kep.
1; neurogenesis; kep.
1; neurogenis; kep.
1; neurogenis; kep.
1; neurogenis; kep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ANK_REPEAT; 4.
; ANK_REP_REGION; 1.
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EGF_1; 34.
EGF_2; 28.
EGF_CA; 22.
   Asx_hydroxyl.
EGF-like.
EGF_2.
EGF_Ca.
EGF_II.
Notch.
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POTENTIAL.
CYTOPLASMIC
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 7.
EGF-LIKE 10.
EGF-LIKE 11.
EGF-LIKE 11.
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EGF-LIKE 12.
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EGF-LIKE 12.
EGF-LIKE 13.
EGF-LIKE 14.
EGF-LIKE 17.
EGF-LIKE 17.
EGF-LIKE 20.
EGF-LIKE 21.
EGF-LIKE 22.
EGF-LIKE 23.
EGF-LIKE 23.
EGF-LIKE 24.
EGF-LIKE 25.
EGF-LIKE 25.
EGF-LIKE 26.
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CALCIUM-
   CALCIUM-BINDING
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                                   4-BINDING
4-BINDING
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(POTENTIAL).
                                                                                                  G (POTENTIAL)
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                                   (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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DISULFID
DISULFI
       \begin{array}{c} 110\\ 110\\ 111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 1111\\ 11
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EGF-LIKE 39.
EGF-LIKE 31, CALCIUM-BIN
EGF-LIKE 31, CALCIUM-BIN
EGF-LIKE 33, CALCIUM-BIN
EGF-LIKE 33, EGF-LIKE 34.
EGF-LIKE 34.
EGF-LIKE 35.
EGF-LIKE 36.
LIN/NOTCH 1.
LIN/NOTCH 1.
LIN/NOTCH 2.
LIN/NOTCH 3.
ANK 2.
ANK 2.
ANK 4.
ANK 5.
ANK 5.
ANK 5.
ANK 5.
ANK 6.
POLY-GLN (OPA-REPEAT).
BY SIMILARITY.
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Matches 303
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                                                                                                VCVCKAGYTGDGIVCLEIN-----PCL----
                                                                                                                                                                                                                                                                                                                  -----SCVHGRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNC-----NGTCH-----
                                                                                                                                                                                                                                                                                                                                             THTCSCLPGETGQTCEHNVDDCTQHACENGGPCIDGINTYNCHCDKHWTGQYCTEDVDE
                                                                                                                                                                                                                                                                                                                                                            NPCANG------GQCSAFESHYICTCPPNFHGQTCRQDVNECAVSPSPCRNGGTCINEV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRCDNNDTIIVRGECG------KCSQQA-PCPLETKPLRETRKCIYSIY 176
----INGYECVCEPGYSGSMCNINIDDCALNPCHNGGTCIDGV----NSFTCLCPDGF-
                    DTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYT
                                                            PLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQ
                                                                                 DGVASFTCDCRPGYTGR--LCETNI-NECLSQPCRNGGTCQDRENAYICTCPKG-----
                                                                                                                             ASTPCKNGAKCTD-GPNKYTCECTPGFSGIH--CELDINECAS----SP---CHYGVCR
                                                                                                                                                                       HCICMPGY--EGVFC-QINSDDCASQPCLNGKCIDKINSFHCECPKGFSGSLCQVDVDEC
                                                                                                                                                                                                                 ECSLGANPCEHGGRCLNTKGSFQCKCLQGYEGPRCEMDVNECKSNPCQNDATCLDQIGGF
                                                                                                                                                                                                                                      ----AINACETSNGGCSTKA--DCK------RTTP-----RTTP-----
                                                                                                                                                                                                                                                          FFCECPHGRTGLLCHLDDACISNPCQKGSNCDTNPVSGKAICTCPPGY--TGSACNQDID
                                                                                                                                                                                                                                                                                                      CELSPNACQNGGTCHNTIGGFHCVCVNGWTGDDCSENI--DDCASAACSHGATCHDRVAS
                                                                                                                                                                                                                                                                                                                                                                                         ----GSYLCRCPPEYTGPHCQR-------LYQPCLPSP-----CRSGGTCVQTS-D
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20.3%;
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7328
7488
7766
7756
804
813
8813
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8843
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8853
8853
8853
8902
9002
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9003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0%; Score 473.5; DB 1; 3%; Pred. No. 3.3e-25; 123; Mismatches 447;
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                                                                                                                                                                                            ---- ENHGG--
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                                                                                                                                                                                                                                      -GNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                    618
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                                                                                                                                                                                                                                                                                                                                                                                                              231
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                                         656
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                                                                                                                                                                                                                                                                                                                          305
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7740 67676777777777777777777777777777777	RC	7 R					os:	n I	DE						NI COL	KESOL	pecit	Db	* 1	04	טט	7	Qy	Db	K	OV	Db	,	Qy	Db	Qy	Db		Qγ	DЬ	į	Οy	Db	Qy	Db	ž	Ov	Db	Š	0	da	Qy)	dd	Qy	Db	Qy	ţ	Db	Qy
MCR 72 PKC 73 PKC 77 PKC 77 PKC 77 CNC 85 CNC 85 CNC 85 CNC 85 CNC 87 CNC 10 CNC 87 CNC 11 CN	STRAIN=ICR X SWISS WEBSTE	SEQUENCE FROM N.A.	Ξ	NCBI_TaxID=10090;	Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mu	Eukarvota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi	Mus musculus (Mouse)	NOTCH3	Neurogenic locus notch 3 protein.	16-OCT-2001 (Rel. 40, Last annotation update	01-NOV-1997 (Rel. 35, Last sequence update	01-NOV-1997 (Rel. 35, Created)	Q61982;	NTC3_MOUSE STANDARD; PRT; 2318		ى ر تا	2	1386 DSPCLVNPCYNGGTCQPISDAPFYRCSCPANFNGLLCHILDYSFSGGQGR 143		1185 SFPSLTN	1343 SCOSTON TO SCORE OF THE SC		1129 KCGANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGYVGDGFSCSGNLLQVLM 118	1297 YTGKRCETVENGCKDTPCKNGGTCAVASNTKHGYICKCQPGYSGSSCEYDSQ 134	+ O O C C C C C C C C C C C C C C C C C	1073OYKLTEDKAKEACAKEAATTATYNOLSYAOKAKYHLCSAGWLESGRVAYPTTVASO 112	1250 GCVCPAGFVGERCEGDVNECLSDPCDPSGSYNCVQLINDFRCECRTG 129		1015 KCECKSHYVGDGVDCEPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHLRSPLG 107	1199 LVNTYKCSCPRGTQGVHCEIDIDDCSPSVDPLTGEPRCFNGGRCVDRVGGY 124	972SCSCKKGYKGDGYSC-IEIDPCADGVNGG-CHEHATCRMTGPGKH 101	1142 EQVDECQPNPCQNGATCTDYLGGYSCECVPGYHGMNCSKEINECLS-QPCQNGGTCID 119	======================================	941DGITCTVVDFCKQNNGGCAKVAKCSQKGTQV- 97	1082 QCASGWTGIYCDVPSVSCEVAARQQGVSVAVLCRHAGQCVDAGNTHLCRCQAGYTGSYCQ 114		896 LCETGWTAASCDTPTAVFAVCTPACSVHATCTENNTCVCNLNYEG 94	1022 ECDSRPCQNGGSCQDGYGTYKCTCPHGYTGLNCQSLVRWCDSSPCKNGGSCWQQGASFTC 10	874 -CQPRSCSEHGQCDEGITGSGEC 89	966 TCSCPAGESGINCEINTPDCTESSCENGGTCVDGISSESCVCLPGETGNYCQHDVN 10		. 846 ТРМСОСТ,СНТСЕРИСТАСЕТ	906 IDDCEPNPCSNGGYCQDRVNGFYCYCLAGFRGERCAEDIDECVSAPCRNGGNCTDCVNSY 96	:	. 831 MODOCACOCC	856 PAGWQGQTCEVDINECVRNPCTNGGVCENLRGGFQCRCNPGFTGALCEND 90	//6 PLKSKPKGVKKKCIYNPLPFRRNVEGCQNLCTVVIQTPRCCHGYF 82		799 -LNOGSCIDDVAGFKCNCMLPYTGEVCENVLAPCSPRPCKNGGVCRESEDFOSFSCNC 85	726 FIHRGLLFDVGVAYGIDCLLMNPTLGGRCDTFTTFDIPGECGSCIFTPKC 77	740 EAGWMGRNCDININECLSNPCVNGGTCKDMTSGYLCTCRAGESGPNCQMNINECASNPC- 79	676KFHVIRDSKALASDLPRSASWKTLQGSEL-SVRCGTGSDIGELFLNEQMCR 72	TOTAL STREET STR	707	619 KFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDELFNQDNKDKLKSYL 675

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R InterPro; IPR002110; ANK.
R InterPro; IPR002110; ANK.
R InterPro; IPR000152; Asx_hydroxyl.
R InterPro; IPR000561; EGF-1ike.
R InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_LI.
InterPro; IPR000800; Notch.
Pfam; PF00023; ank: 6
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PRINTS; PRO1452; NG
SMART; SM00248; AN
SMART; SM00001; EGI
SMART; SM00001; EGI
SMART; SM00001; EGI
SMART; SM00004; NL;
PROSITE; PS50088; /
PROSITE; PS50029; /
PROSITE; PS0010; /
PROSITE; PS00022; PROSITE; PS01186; /
PROSITE; PS01187; I
PROSITE; PS01187; I
PROSITE; PS01187; I
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Lardelli M., Dalstrand J., Lendahl U.;
"The novel Notch homologue mouse Notch growth factor-repeats and in
   TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth factor-repeats and is expressed
neuroepithelium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H. Dev. 46:123-136(1994).

FUNCTION: NOTCH 1, 2 AND 3 PLAY A COMBINATIONAL ROLE DURING FUNCTION: CELL FATE DECISIONS AND MORPHOLOGICAL MOVEMENTS IN TO DEVELOPING CNS AND PROBABLY OTHER REGIONS OF THE EMBRYO.

TISSUE SPECIFICITY: PROLIFERATING NEUROEPITHELIUM.
DEVELOPMENTAL STAGE: CNS DEVELOPMENTS.
SIMILARITY: CONTAINS 34 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     m; pF00023; ank; 6.
m; pF00008; EGF; 34.
m; pF00006; notch; 3.
nr; pF00010; EGFBLOOD.
nrs; pF001010; EGFBLOOD.
nrs; pF001452; NOTCH.
nr; SM00179; EGF_CA; 19.
nr; SM00001; EGF_LIKe; 13.
nr; SM00004; NL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X74760; CAA52776.1;
P00740; 1IXA.
     Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANK_REPEAT; 4.
ANK_REP_REGION;
ASX_HYDROXYL; 18
EGF_1; 33.
EGF_2; 27.
EGF_CA; 17.
   1643
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 CYTOPLASMIC.
PEST.
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 5.
EGF-LIKE 5.
EGF-LIKE 10.
EGF-LIKE 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat;
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in proliferating
                                   CALCIUM-BINDING
CALCIUM-BINDING
CALCIUM-BINDING
CALCIUM-BINDING
CALCIUM-BINDING
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CALCIUM-BINDING
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                                   (POTENTIAL).
(POTENTIAL).
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-GIRCESQV-DECRSQP--CRYGGKCLDLVDKYLCRCPPGT
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No. 3.
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SEQUENCE FROM N.A.
TISSUE=Schwann cell;
MEDLINE=92111383; PubMed=1764995;
Weinmaster G., Roberts V.J., Lemke
"A homolog of Drosophila Notch expr
development.";
                                                                                                                     NTC1_RAT
Q07008;
Q07008;
01-NOV-11995
15-JUL-11999
16-OCT-2001
Neurogenic L
                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
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                                                                                                                             i (Rel. 32, Created)
(Rel. 38, Last sequence update)
(Rel. 40, Last annotation update)
Locus notch homolog protein 1 precursor.
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                                                                                      ; (Rat).
Da; Chordata;
La; Rodentia;
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                          Lemke
                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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               expressed
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               mammalian
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Interpro; IPRO00552; Asx_hydroxyl.
Interpro; IPRO00561; EGF-11ke.
Interpro; IPRO00742; EGF-2.
Interpro; IPRO001881; EGF-Ga.
Interpro; IPRO01881; EGF-Ga.
Interpro; IPRO02049; Laminin_EGF.
Interpro; IPRO02049; Laminin_EGF.
Interpro; IPRO002049; Notch.
pfam; PF00023; ank; 6.
Pfam; PF00008; EGFBLOOD.
Pfam; PF00010; EGFEAMININ.
PFANTS; PRO0011; EGFEAMININ.
PRINTS; PR00011; EGFEAMININ.
PRINTS; PR00179; EGF_CA; 25.
SMART; SM00179; EGF_CA; 25.
SMART; SM00004; NL; 2.
SMART; SM000004; NL; 2.
PROSITE; PS50098; ANK_REP_REGION; 1.
PROSITE; PS000010; ASX_HYDROXYL; 22.
PROSITE; PS000186; ASX_HYDROXYL; 22.
PROSITE; PS00010; ASX_HYDROXYL; 22.
PROSITE; PS0001187; EGF_CA; 21.
Differentiation; Neurogenesis; Repear
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Submitted (APR-1998) to the
-!- FUNCTION: REQUIRED FOR GOT TISSUES:
-!- SUBCELLULAR LOCATION: TO
-!- DEVELOPMENTAL STAGE: IN
DAYS 12 AND 14 AND DECR
   Transmembrane;
SIGNAL 19
CHAIN 19
CHAIN 19
DOMAIN 1724
DOMAIN 1724
DOMAIN 20
DOMAIN 102
DOMAIN 102
DOMAIN 174
DOMAIN 257
DOMAIN 257
DOMAIN 257
DOMAIN 257
DOMAIN 257
DOMAIN 335
DOMAIN 372
DOMAIN 412
DOMAIN 452
DOMAIN 456
DOMAIN 568
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HSSP; P00740; 1IXA.
InterPro; IPR002110; ANK.
InterPro; IPR000152; ASX_F
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SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE F
SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                     Signal;
                                                                                                                                                                                                                                                                                                                                                                                                   Neurogenesis; Repeat; ignal; Glycoprotein.
     OCATION: Type I membrane protein
STAGE: IN THE EMBRYO, HIGHEST LI
4 AND DECREASE RAPIDLY TO MUCH LA
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POTENTIAL.

NEUROGENIC LOCUS NOTCH HOMOL
EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

EGF-LIKE 1.

EGF-LIKE 2.

EGF-LIKE 5.

EGF-LIKE 5.

CALCIUM-BINDING
EGF-LIKE 6.

EGF-LIKE 7.

CALCIUM-BINDING
EGF-LIKE 10.

EGF-LIKE 11.

EGF-LIKE 11.

CALCIUM-BINDING
EGF-LIKE 12.

CALCIUM-BINDING
EGF-LIKE 13.

CALCIUM-BINDING
EGF-LIKE 14.

CALCIUM-BINDING
EGF-LIKE 15.

CALCIUM-BINDING
EGF-LIKE 16.

CALCIUM-BINDING
EGF-LIKE 17.

CALCIUM-BINDING
EGF-LIKE 18.

CALCIUM-BINDING
EGF-LIKE 19.

CALCIUM-BINDING
EGF-LIKE 11.

CALCIUM-BINDING
EGF-LIKE 15.

CALCIUM-BINDING
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DGPNTYTCVCTEGYTGTHCEVDIDECDPDPCHIGLCKDGVATFTCLCQPGYTGHHCETNI
                         AGPGPFTVFAPLSSSFNH-EPRIKDWD-----
                                                                 GCSPFAFCNYTEQDQRICTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVREL
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275; Conser
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21.5%;
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LCQCPKGFSGH--LCQYDV-DECAST
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                                     Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
                                                                                          _MOUSE MOUSE STANDARD; PRT; 2531 AA. O1705; O1-NOV-1995 (Rel. 32, Created) O1-FEB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Neurogenic Locus notch homolog protein 1 precursor NOTCH1 OR MOTCH.
 [1]
SEQUENCE FROM |
TISSUE=Embryo;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVRWC--DSAPCKNGGKCWQTNTQYHCECRSGW--TGFNC
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                                                      Chordata;
Rodentia;
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                                                    Craniata; Ver
Sciurognathi;
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                                                      Vertebrata;
thi; Muridae;
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                                                       Murinae;
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pfam; pfu,

pfam; pfu,

pfam; pfo006,

R pfam; pf0006,

PR prints; pr00010;

DR prints; pr001452; NO1.

DR SMART; SM000179; EGF_CA; 23.

DR SMART; SM000179; EGF_like; 11.

DR SMART; SM00004; NL; 2.

PROSITE; pS00001; EGF_like; 11.

PROSITE; pS00001; AKK_REP_REGION; 1.

PROSITE; pS00010; ASX_HYDROXYL; 22.

PROSITE; pS01186; EGF_1; 34.

"STITE; PS01186; EGF_2; 27.

"STORE PS01187; EGF_CA; 21.

"Ation; Neurogenesis

"Signal; Glycc

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                 TITITITITITITITITITITIVEEN RARRARAK
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C MEDLINE-93048835; PubMed-1425352;

A Franco del Amo F., Smith D.E., Swiatek P.J., Gendron-Mag A Franco del Amo F., Smith D.E., Gridley T.;

A Greenspan R.J., McMahon A.P., Gridley T.;

T "Expression pattern of Motch, a mouse homolog of Drosoph suggests an important role in early postimplantation mou development.";

Development 115:737-744(1992).

C -!- SUBCELULAR LOCATION. Type I membrane protein.

C -!- SUBCELULAR LOCATION. Type I membrane protein.

C -!- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.

C -!- SIMILARITY: CONTAINS 3 LIN/NOTCH ROPEATS.

C -!- SIMILARITY: CONTAINS 3 AIN REPEATS.

C -!- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.
             Transmembrane;
SIGNAL 19
CHAIN 19
DOMAIN 1726
DOMAIN 1747
DOMAIN 102
DOMAIN 102
DOMAIN 102
DOMAIN 102
DOMAIN 102
DOMAIN 1140
DOMAIN 1140
DOMAIN 178
DOMAIN 218
DOMAIN 218
DOMAIN 219
DOMAIN 257
DOMAIN 295
DOMAIN 335
DOMAIN 335
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between
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Franco del Amo F., Gendron-Maguire M., Swiatek P.J., Jenkins N.A.,
Copeland N.G., Gridley T.;
"Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of Drosophila Notch.";
Genomics 15:259-264(1993).
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InterPro;
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InterPro;
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protein INT-3).
NOTCH4 OR INT3 OR INT
Mus musculus (Mouse).
Eukaryota; Metazoa; C

OR INT-3.

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

precursor

(Transforming

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pfam; pF00023; ank; 6.
pfam; pF00008; EGF; 27.
pfam; pF000068; EGF; 27.
pfam; pF000068; EGF; 27.
pfam; pF000068; DCGF; 22.
prints; pr00145; ANKYRIN.
prints; pR00145; NOTCH.
SMART; SM00248; ANK; 5.
SMART; SM00001; EGF_Like; 15.
SMART; SM00001; EGF_Like; 15.
SMART; SM00001; AIK_REPEAT; 5.
pROSITE; pS50098; ANK_REPEAT; 5.
pROSITE; pS50010; ASK_HYDROXYL; 11.
pROSITE; pS001010; ASK_HYDROXYL; 11.
pROSITE; pS001187; EGF_L; 28.
pROSITE; pS011187; EGF_CA; 9.
Differentiation; Neurogenesis; Repeat Glycoprotein; Proto-oncogene; ANK reprosition of the control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M80456; AAB3837
EMBL; U43691; AAC5263
PIR; A3072; TVMVT3.
HSSP; P08709; IBF9.
MGD; MGI:107471; Notcl
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between
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Development 122:2251-2259(1996).

-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- DISEASE: ACTIVATED INT-3 TRANSFORMS MAMMARY EF.
-i- SIMILARITY: CONTAINS 29 EGF-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
-i- SIMILARITY: CONTAINS 5 ANK REPEATS.
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Uyttendaele H., Marazzi G., Wu G., Yan Q
"Notch4/int-3, a mammary proto-oncogene,
cell-specific mammalian Notch gene.";
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MEDLINE=97294599; PubMed=9150355;
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"Mouse mammary tumor gene int-3: a member
transforms mammary peithelial cells.";
J. Virol. 66:2594-2599(1992).
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NCBI_TaxID=10090;
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mouse mammary tumor associated
NOTCH gene family (NOTCH4).";
gene 14:1883-1890(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                   5; IPR002110; ANK.
5; IPR000152; Asx_hydroxyl.
5; IPR000761; EGF-like.
5; IPR000742; EGF_2.
6; IPR001881; EGF_Ca.
6; IPR001438; EGF_II.
6; IPR000800; Notch.
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AAC52630.1; -.
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                                                                                                                                                                      Rowen L.,
Banta A.,
                                                                                                                                                                                                                                                                                                                                                                  P22105; P78530; P78531; Q08424; Q9UMG7; 01-AUG-1991 (Rel. 19, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Tenascin-X precursor (TN-X) (Hexabrachion-like). TNXB OR TNX OR XB OR HXBL.
                                                                                                                  "Sequence
locus.";
                                                                                                                                                                                                                                                                                                                                                TNXB
Homo
                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1003
                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TENX_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIDLCARKPCPHTARCLQS-GPSFQCLCLQGWTGALCDFPLSCQMAAMSQGIEISGLCQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTPRCCHGYFMPDCQACPGGPDTPCNNRGMCRDLYTPMG-OCLCHTGFNGTACELCWHGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVDHCVSASCLNGGTCVNKPGTFFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLTCSEEVTACHSGP-----CLNGGSCSIRPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VDECL--DRPCHPSGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLDRCLQDNGQCHPDASCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAPGYEGQNCSKV-LEACQ---SQPCHNHGTC-TSRPGGFHCACPPGFV--GLRCEGD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGLCIDTGSSYFCRCPPGFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTP-TAVFAVCTPACSVHATCTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGLHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGVAYGIDCLLMNPTLGGR-CDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VT---VFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWK 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGQLC-EVPLCTPNMCQPGQQCQGQ-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFCNYTEQDQRICTCKPDYTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTTFDIPGEC---GSCIFTPK---CPLKSKPKGVKKKCIYNPLPFRRNVEGCQNLCTVVI
                                                                                                                                          FROM N.A.

Dankers C., Baskin D., Faust J., I
Schwartzell S., Smith T.M., Spies
determination of 300 kilobases of
                                                                                                                                                                                                                                                                                                                                           (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCEKEVDECLSDP-----CPVGASC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEKTNPSCADSPCRNKATCQD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -CNLNYEGDGITCTVVDFCKQNNGGCA----KVAKCSQKGTQVSCS
                                                                                                                                                                                                                                                                                                 Primates;
                                                                                                                                                                                                                                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1018
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                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLCQDNMNPCEPNPCHHGSTCVPQPSGYVCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -TPRGARCLCSPGYTGSSCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                          Loretz C.,
es T., Hood L
of the human
                                                                                                                                                                                                                                                                                              Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -EHRAPCLCPD - -GSPGCVPAED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -YSCTCL---PSHTGRHCQT
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                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LCATGF
                                                                                                                                                                                              Z
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                                                                                                                                                 MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              763
```

[2]
SEQUENCE OF 1-747 A
TISSUE=Leukocyte;
MEDLINE=93300909; F

AND

1687-1944 FROM the

z

to

EMBL/GenBank/DDBJ

databases

PubMed=7686164;

```
MEDLINE-09367293; PubMed=2475872;

RA MOTELY () B15120W J. Gitelman S.E., Miller W.L.;

RA MOTELY () B15120W J. Gitelman S.E., Miller W.L.;

RT "Transcript encoded on the opposite strand of the human ster

Thydroxylase/complement component C4 gene locus.";

Thydroxylase/complement component C4 gene locus.";

C PIONCTION: APPEARS TO MEDIATE INTERACTIONS BETWEEN CELLS;

EXTRACELLULAR MATRIX. SUBSTRATE-ADHESSION MOLECULE THAT AF

EXTRACELLULAR MATRIX. SUBSTRATE-ADHESSION MOLECULE THAT AF

OF EPITHELIAL TUMORS.

1-1- SUBCELLULAR LOCATION: EXTRACELLULAR matrix.

1-1- SUBCELLULAR LOCATION: EXTRACELLULAR matrix.

1-1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; XB (SHOWN HERE)

XB-SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.

1-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL ADRENAL, IN

TESTIS, FETAL SMOOTH, STRIATED AND CARDIAC MUSCLE. XB-SHOR ONLY EXPRESSED IN THE ADRENAL GLAND.

1-1- DISBASE: ASSOCIATION WITH COMPONENTS.
                                                                                                                                                                                                                                                                                                                                                        modified
entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tee M.K., Thomson A.A., Bristow J., Miller W.L.;
"Sequences promoting the transcription of the human
overlapping P450c2la correctly predict the presence
adrenal-specific, truncated form of tenascin-X.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96015044; Pub
Tee M K mi-
                                                                              InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Fetal adrenal gland;
MEDLLNE=97081760; PubMed=923003;
Speek M., Barry F., Miller W.L.;
Speek M., Barry F., Miller W.L.;
"Alternate promoters and alternate splicing of gene with 5' and 3' ends buried in other genes."
Hum. Mol. Genet. 5:1749-1758(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adrenal-specific, truncated Genomics 28:171-178(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM XB-SHORT). TISSUE=Adrenal gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bristow J., Tee M.K., Gitelman S.E., merron, ..., ..... Transcin-X: a novel extracellular matrix protein encoded by the human Transcin-X: a novel extracellular matrix protein encoded by the human Transcin-X: gene overlapping P450c21B.";

J. Cell Biol. 122:265-278(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISEASE: ASSOCIATION WITH CONGENITAL ADRENAL HYPERPLASIA DISEASE: Defects in TNXB are a cause of autosomal recess Ehlers-Danlos syndrome.

Ehlers-Danlos syndrome.

SIMILARITY: CONTAINS 19 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 32 FIBRONECTIN TYPE III-LIKE DOMAIN SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL THE BETA AND GAMMA CHAINS OF FIBRINOGEN.

CAUTION: THERE ARE TWO GENES FOR TN-X: TNXA AND TNXB. TN A PARTIAL GENE WHICH CAN SOMETIME RECOMBINE WITH TNXB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINE=96015044; PubMed=8530023; M.K., Thomson A.A., Bristow J
erPro: IPR000561; EGF-like.
erPro: IPR003961; FN_III.
erPro: IPR002181; Fibrinogen_C.
erPro: IPR002049; Laminin_EGF.
n; PF00147; fibrinogen_C; 1.
n; PF00041; fn3; 6.
                                                                                                                                                       European
                                                                                                                       600985;
606408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry
                                                                                                                                                                                                                                                                                                                                                          an
                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ROT entry is copyright. It is produced through Swiss Institute of Bioinformatics and the El Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASSOCIATION WITH CONGENITAL ADRENAL HYPERPLASIA. Defects in TNXB are a cause of autosomal recessive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.A
                                                                                                                                                                                                                                                                                                 .'
                                                                                                                                                                                                                                                                                                                                                                                                                  as its content
                                                                                                                                                                                                                                                                                                                                                                            http://www
                                                                                                                                                                                                                                                                                                                                                                                                Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETWEEN CELLS AND THE OLECULE THAT APPEARS SUPPORTING THE GROWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human tenascin-X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XA gene
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RMINAL PART
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PROSITE; PS01186; EGF_2; 19.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN;
Glycoprotein; Cell adhesion; Repeat;
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SM00181; EGF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 GCQPQCVRTIITRACWLASLAHNAKPAPGEV---KMCALGTASVWDGVNGTGTCQCGLGF 242
                                                                                                                                                                                                                                                                                 DIPGECGSCIFTPKCPLKSKPKG--VKKKCIYNP-----LPFRRNVEGCQ--NLCTVVI 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITD-----SIHTPVTVFW 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLKEQC-----TGGCCPAS----AQAGTGQTDVRTLCSL--HGVFD--LSRCTCSCEPGW 162
GQEEPPASACPGGCGPRELCR-----AGQCVCVEGF--RGPDCAIQTCPGD--CRGRGEC
                                                                                                                          --GVRQCPNDCSQHGVCQDGV-----CICWEGYVSEDCSIRT-----CPSNCHGRGRC-E
                                                                                                                                              RFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVHATCTE
                                                                                                                                                                                                              QTPRCCHGYFMPDC--QACPGGPDTPCNNRGMCRDLYTPMGQCLCHTGFNGTACELCWHG 868
                                                                                                                                                                                                                                                       CWPGYTGRDCGTRACPGDCRGRGRCVDGRCVCNPGFTGEDCGSRRCPGDCRGHGLCEDGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGW----PSCPGDCQGRGRCV----QGVCVCRAGF--SGPDCSQ-RSCPR---GCSQRG
                            IEIDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDCEPEQLPLDRCLQDNGQC
                                                                                            NNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKG--TQVSCSCKKGYKGDGYSC 986
                                                                                                                                                                                         CV--CDAGYSGEDCSTRSCPGG----CRGRGQCLD-----GRCVCEDGYSGEDC-----
                                                                                                                                                                                                                                                                                                                     -----RCENGVCV------CNAGYSG--EDCGVRSCPGDC-----RGRGRCESGRCM 482
                                                                                                                                                                                                                                                                                                                                                                                     PGYTGTDCGSRACP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----CPRDCRGRCEDGECICDTGYSG-----DDCGVRSCPGDCNQRGRCEDGRCVCW 422
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                                                             -TC-ATRMCP
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N-LINKED (GLCNAC. . .) (POTENTIAL).
MISSING (IN ISOFORM XB-SHORT).
G -> GEOG (IN REF 2).
P -> G (IN REF. 3 AND 5).
M -> I (IN REF. 3 AND 5).
M -> I (IN REF. 3 AND 5).
                                                            -ADCRGRGRCVQGVCLCHVGYGGE--DC
                                                                                                                                                                                                                                                                                                                                                                                     -- RDCRGRG
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Search completed: June 17, 2002, 12:35:32 Job time: $308 \ \text{sec}$

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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US-08-08-32-384-19
US-08-611-729A-10
US-08-611-729A-10
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US-08-611-729A-10
US-08-611-729A-6
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US-08-68-740A-7
US-09-068-740A-7
US-09-068-740A-7
US-09-068-740A-11
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13, Appl
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16, Appl
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19, A
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T07-#36-	TOPOLOG MOLECULE	: LENGTH: 2523 amino acids	INFORMATION FOR SEQ ID NO: 18:	TELEPHONE: (212) /90-9090 TELEFAX: (212) /869-8864/9741 TELEFAX: 661/1 DENNITE	TELECOMMUNICATION INFORMATION:	1	NAME: MISTOCK S LOSTID	FILING DATE: 21-JAN-1994 CLASSIFICATION: 530	08/185,432	<pre>; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: PatentIn Release #1.0, Version #1.30</pre>	disk patible	COMPUTER READABLE FORM:	COUNTRY: U.S.A.	; CITY: New York ; STATE: New York	1	ADDRESS:	TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS	suno, Kenji TON: DELTEX PROTETNS	derich Tian	seau, Isabel	NATION:	RESULT 1 US-08-185-432-18 ; Sequence 18, Application US/08185432	ALIGNMENTS	5 276.5 3.5 833 2 US-08-346-126-	3 276.5 3.5 833 1 US-08-083-590 <i>t</i> 4 276.5 3.5 833 1 US-08-465-500-	2 276.5 3.5 833 1 US-08-264-534-	0 279 3.5 713 3 US	7 322 4.1 1525 3 US-09-191-647- 8 322 4.1 1525 4 US-09-540-2457-	US95-11684 US95-11684	3 337.5 4.3 3075 2 US-08-125-07	1 339.5 4.3 1248 4 US-08-882-046-6 2 337.5 4.3 3075 2 US-08-460-309-5	9 341.5 4.3 1212 4 0S-09-214-27 0 341.5 4.3 1257 3 0S-08-611-72	8 341.5 4.3 1055 4 US-09-214-27
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Query Match
Best Local Similarity
Matches 302; Conserv

Conservative

131;

Mismatches

Indels 486;

Gaps

93;

6.2%; Score 486; DB 1 21.9%; Pred. No. 8e-31;

DB 1; Length 2523;

974	9 ACSVHATCTENNTCVCNLNYEGDGITC-TVVDFCKQNNGGCAKVAKCSQKGTQVSCS	ОУ 91	
1027	6 GIHCESNTPDCTESSCFNGGTCIDGI-NTFTCQCPPGFTGSYCQHDINECDSK	Db 97	
918	GTACELCWHGREGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVCTP	Qy 85	
975	CSDGINMFFCN-CPAGFRGPKCEEDINECASNPCKNGANCTDCVN	Db 921	
858	1	Оу 818	
920	NGATCQNTNGSYKCNCKPGYTGRNCEMDIDDCQPNP	Db 879	
817	KCPLKSKPKGVKKKCIYNPLPFRRNVEGCQNLCTVVIQTPRCCH	Оу 774	
878	PYTGAICEAVLAPCAGSPCKNGGRCKESEDFETFSCECPPGWQGQTCEIDMNECVNRPCR	Db 819	
773		Qy 746	
818	GGTCKDMTGAYICT-CKAGFSGPNCQTNINECSSNPCLNHGTCIDDVAGYKCNCML	Db 764	
745	SASWKTLQGSELSVRCGTGSDIGELFLNEQMCRF	Оу 693	
763	GVNGYKCDCEAGWSGSNCDINNNECESNPCMN	Db 732	
692	PVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDS	Qу 640	
731	NPCRNGGTCKDQINGFTCVCPDGYHDHMCLSEVNECNSNPCIHGACHD	Db 684	
639	TPKDALGRVLQNLTTVAANHGYTKFSKLI	Qy 596	
683	TCPKGTTGVNCETKIDDCASNLCDNGKCIDKIDGYECTCEPGYTG	Db 627	
595	SVSQDTVFINNEAKVLSSDIISTNGVIHVI	Qy 555	
626	NECIPDPCHYGTCKDGIATFTCLCRPGYTGRLCDNDINECLSKPCLNGGQCTDRENGYIC	Db 567	
554		Qy 507	
566	KINEFRCDCPTGFSGNLCQHDFDECTSTPCKNGAKCLDGPNSYTCQCTEGFTGRHCEQDI	Db 507	
506	STSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNH	Qy 472	
506	NECLSNPCQNDSTC-LDQIGEFQCICMPGYEGLYCETNI-DECASNPCLHNGKCID	Db 453	
471	NVCLTNNGGCSPFAFCNYTEQDQRICTCKPDYTGDGIVCRGSIYGELPKNP	Qy 421	
452	ACNNDVDECSIGANPC EHGGRCTNTLGSFQCNCPQGYAGPRCEIDV	Db 404	
420	TGDGIVC-LEINPCLENHGGCDRNAECTQT-GPNQAVCNCLPKYTGDGKVCSL-I	Qу 369	_
403	-HDRVASFYCECPHGRTGLLCHLDNACISNPCNEGSNCD-TNPVNGKAICTCPPGY	Db 350	
368	DPDGKAS CKCAAGERGNGTVCTAINACETSNGGCSTKADCKRTTP GNRVCVCKAGY	Qy 313	_
349	DVDECQLMPNACQNGGTCHNTYGGYNCVCVNGWTGEDCSENI DDCANAACHSGATC	Db 294	
312	L	Qy 264	_
293	PSNNCRNGGTCVDGVNTYNCQCPPDWTGQYCTE	Db 234	_
263	TCTEGKYGIHCDQAC	Оу 238	_
233	NGGQCINEFGSYRCTCQNRFTGRNCDEPYVPCNPSPCLNG-GTCR	Db 190	_
237	AKPAPGEVKMCALGTASVWDGVNGTGTCQ	Qy 190	~
189	SCQQADPC ASNPCANGGKCLPFEIQYICKCPPGFHGATCKQDINECSQNPCK	Db 138	-
189	RSVFIGCQP	Qy 151	~
137	FICHCPVGFTDKVCLTPVDNACVNNPCRNGGTCELLNSVTE-YKCRCPPGWTGD	Db 85	_
150	VRGECG	Qy 105	_

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; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: unknown
; MOLECULE TYPE: pepti
US-08-083-590A-20
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Patent No. 5786158
                                                                                                                        Query Match
Best Local Similarity
Matches 269; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083
FILING DATE: 25-JUN-1993
FILING DATE: 25-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION UNMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEPHONE: 212 8098864/9741
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                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2556 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Artavanis-Tsakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
TITLE OF INVENTION: Nucleic Acids
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 10036
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                                          ENIDDCPGNNCKNG-----GACVDGVNTYNCPCPPEWTGQYCTEDVDECQLMPNACQNG 309
                                                                                EKVLEIQKNRCDNNDTIIVRGEC--GKCSQQAPCPLE-----TKPLRETR------
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    -KCIYSIYFMGKRSVFIGCQPQCVRTI---ITRACWLASLAHNAK----- 210
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                                                                                                                                           6.1%; Score 480.5; DB 1
21.7%; Pred. No. 2.3e-30;
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                                                  --SPCQNGATCTDY-----LGGYSCKCVAGYHGVNCSEEIDECLS------
                                                                                   DNGQCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYA
                                                                                                                                                                                                                    NLNYEGDGITC-TVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKG-----DGYSCIE
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                                                                                                                  VAAQRQGVDVARLCQHGGLCVDAG-NTHHCRCQAGYTGSYCEDLVDECSP-
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GENERAL INFORMATION:
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Sequence 20, Apprix
0. 6083904
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FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 08/083,590
APPLICATION NUMBER: 25-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212 8698864/
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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LENGTH: 2556 amino acids
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TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
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TITLE OF INVENTION:
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STATE: New Yor
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mes 269; Conserv
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                                                        YGIHCDQACSCVHGRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNC-NGTCHTSANCLLD
                                                                                                                                                                                                                                                                       GTCHNTHGGYNCVCVNGWTGE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGGCSPFAFCNYTEQDQRI----CTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQE 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTGH--LCQYDVDECAST--PCKNGAKCLD-GPNTYTCVCTEGYTG-----THCEVD 566
                                                                                                                                                                                                                    VAAQRQGVDVARLCQHGGLCVDAG-NTHHCRCQAGYTGSYCEDLVDECSP------
                                                                                                                                                                                                                                                                                                                                                                                                CSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVC-TPACSVHATCTEN---NTCVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QN\hbox{------}THGGYRCHCQAGYSGRNCETDIDDCRPNPCHNGGSCTDGINTAF--C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----HGACRDSLNGY-KCDCDPGWSGTNCDINNNECESNPCVNGGTCKDMT-SGIVCT 778
                                   WDVFCY-----RMKDVNCTCKAGYVGDGFSCSGNLLQVL 1183
                                                                                                                                            --SPCQNGATCTDY-----LGGYSCKCVAGYHGVNCSEEIDECLS------
                                                                                                                                                                                                                                        PQGYTGP--NCQNLVHWC--DSSPCKNGGKCWQTHTQYRCECPSGWTGLYCDVPSVSC-E 1103
                                                                                                                                                                                                                                                                                                                         NLNYEGDGITC-TVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKG-----DGYSCIE
                                                                                                                                                                                                                                                                                                                                                                 CFNGGTCVDGI-NSFTCLCPPGFTGSYCQ---HVVNECDSRPCLLGGTCQDGRGLHRCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                        DCLPGFRGTFCEEDINECASDPCRNGANCTDCVDSYTCTCPAGFSGIHCENNTPDCTESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDGI-----NGFTCRCPEGY-----HDPTCLSEVNECNSNPCV--
----CFNNGTCVDQVGGYSCTCPPGFVGE--RCEGDVNECL 1273
                                                                                                           QKAKYHLCSAGWLESGRVAYPTTYASQKCGANVVGI-------VDYGSRANKSEM 1149
                                                                                                                                                                                DNGQCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYA 1101
                                                                         ---HPCQNG---GTCLDLPNTYKC-SCPRGTQGVHCEINVDDCNPPVDPVSRSPK---
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RESULT 4 US-08-185-432-19 ; Sequence 19, Ap

Application US/08185432

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GENERAL I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2703 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Artavanis
APPLICANT: Busseau,
APPLICANT: Diederich
APPLICANT: Xu, Tian
APPLICANT: Matsuno,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCE.
CORRESPONDENCE ADDRESS:
PENNIE & EDMONDS
AMERICA OF The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 18
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 21-JAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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                                                                                                                                                                                                                                                                                         KCAAGFRGNGTVC-TAINACETSNGGCSTKADCKRTTPGNRVCVCKAGYTG-----DGIV 374
                                                                                                                                                                                    C-QSNPCL-NDGTCHDKINGFKCSCALGFTGARCQINIDDCQSQPCRNRGICHDSIAGYS
                                                                                                                                                                                                         CLEINPCLENHGGC-DR-----
                                                                                                                                                                                                                                                                                                                                                                                                       KDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAKVL 570
                                                                                                            CECPPGYTGTS -- CEININDCDSNPCHRGKC -- -- -IDDVNSFKCLCDPGYT -- GYIC
                                                                                                                                              --CLPKYTGDGKVCSL-INVCLTN---NGGCSPFAFCNYTEQDQRICTCKPDYTGDGIVC 459
                                                                                                                                                                                                                                                          NCSQGF--TGPRCETNINECESH--PCQNEGSC-LDDPGTFRCVCMPGFTGTQCEIDIDE 529
                                                                                                                                                                                                                                                                                                                                CHADAICDTSPINGSYACSCATGYKGVDCSEDI--DECDQGSPCEHNGICVNTP-GSYRC
                                                                                                                                                                                                                                                                                                                                                                   C-VHGRCSQGPL-GDGSCDCDVGWRGVKCDMEITTDNCN--GTCHTSANCLLDPDGKASC
                                    QKQI-NECESNPCQFDGHCQDRVGSYYCQCQ-----AG-----TSGKNCEVNV
                                                                        RGSIYGELPKNP-----STSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRI 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2703 amino acids
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Busseau, Isabelle
Diederich, Robert J.
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(212) 869-8864/9741
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N. 520
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DELTEX PROTEINS, NUCLEIC ACIDS, AND
ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
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US-08-185-432-17
                                                                                                                                                                                                                                                                                                                                    Patent No. 5750652 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/08185432 Patent No. 5750652
                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                  APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTE:
TITLE OF INVENTION: ANTIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1149
                                                                                                      CORRESPONDENCE ADDRESS:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1283 CVCQPGFV--GARCEGDINECL 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1162 CTCKAGYVGDGFSCSGNLLQVL 1183
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                                                                                                                                  NUMBER OF SEQUENCES:
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                            ADDRESSEE: PENNIE & EDMONDS STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               783 GVKK-----KCI--YNPLPFR-----
       STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CQNGGTCHDRV----MNFSCSCPPGTMGII---CEINKDDCKPGACHNNGSCIDRVGGFE 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSAGWLESGRVAYPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCY-----RMKDVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIDCLLMNPTLGGRCDTFTTFDIPGEC---GSCI-----FTPK-CPLKSKPK 782
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       New York
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                                                                                                                                                                                                                                                                                  Busseau,
                                                                                                                                                                                                                                   Xu, Tian
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                                                                                                                                                          COMPOSITIONS
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; MOLECULE TYPE:
US-08-185-432-17
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Matches 262;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 2556 amino aci
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ALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRC----
                                                                                                                                                                                                                                                                                        LLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKN 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QIGEFQCMCMPGYEG---VHCEVNTDECASSPCLHNGRCLDKIN-----EFQCECPTG
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                                                                      ---TCEDGI-----NGFTCRCPEGY-----HDPTCLSEVNECNSNPCV------
                                                                                                                                          LLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDECDPDP-CHYGSCKDGVATFTCLCRPGYTGHHCETNINECSSQPCR--LWGTC-QDPD 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PAPGEVKMCALGTASV------WDGVNGTGTCQCGLGFNGTAC----ETCTEGK 254
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(212) 869-8864/9741
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Pred. No. 1.3e-29;
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ZIP: 1003b-z/--
ZIP: 1003b-z/--
ZIP: 1003b-z/--
COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
REDIUM TYPE: FLOOPPATIBLE
COMPUTER: IBM PC compatible
COMPUTER: FSTEM: PC-DOS/MS-DOS
There #1.0
                                                                                                                                                                                                                                                         APPLICANT: Xu, Tian
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTE
TITLE OF INVENTION: ANTIB
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APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
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                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                               STREET: 1155 AVE
CITY: New York
STATE: New York
COUNTRY: U.S.A.
CIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GANVVGIVDYGSRANKSEM-------WDVFCY-----RMKDVNCTCKAGYVG 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYASQKC 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGFSCSGNLLQVL 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SC-----PWGTQGVHCEINVDDCNPPVDPVSWSPKCFNNGTCVDQVGGYSCTCPPGFVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRCQAGYTGSYCEDLVDECSP-----SPCQNGATCTDY-----LGGYSCKCV 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---HVVNECDSRPCLLGGTCQDGRGLHRCTCPQGYTGP--NCQNLVHWC--DSSPCKNGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCIDDVAGYKCNCLL--PYTGATCEVVLAPCAPSPCRNGGECRQSEDYESFSCVCP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KCWQTHTQYRCECPSGWTGLYCDVPSVSC-EVAAQRQGVDVARLCQHGGLCVDAG-NTHH 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCSQKGTQVSCSCKKGYKG-----DGYSCIEIDPCADGVNGG--CHEHATCRMTGPGKHK 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPTAVFAVC-TPACSVHATCTEN----NTCVCNLNYEGDGITC-TVVDFCKQNNGGCAKVA 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TAGAKGQTCEVDINECVLSPC---WHGASCQN-----THGXYRCHCQAGYSGR 903
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                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
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                                                                                                                                                                            E: PENNIE & EDMONDS
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ANTIBODIES, AND R.
23
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Best Local (
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2471 amino aci
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 LYVPCAPSPCVNGGTCRQ--TGDFTFECNCLPGFEGSTCERNI--DDCPNHRCQNGGVCV 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 RKCIYSIYFMGKRSVFIGCQPQCVRTIITRACWLASLAHNAKPAPGEVKMCALGTASVWD 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 GVNGTGTCQCGLGFNGTACET------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 EKNRCQNGGTCVAQAMLGKATCRCASGFTGEDCQYSTSHPCFVSRPCLNGGTCHMLSRDT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity nes 270; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,8
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                                                                                                                                                             DIDDCSS-----TP-----CLNGAKCIDHPNGYECQCATGFTGVLCEENIDNCDPDPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCSPFAFCNYTE-QDQRICTCKPDYTG-----DGIVCRGSIYGELPKNPSTSQYFFQ 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGIVCLEINPCLENHGGCDRNAECTQTG---PNQAVCNCLPKYTGDGKVCSLINVCLTNN 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVANQFSCKCLTGFTGQKCETDVNECDIPGHCQHGGTCLNLPGSYQCQCPQGFTGQYCDS 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YECTCQVGFTGKE-----CQ------WTDAC----LSH------PCANG--STCT 160
                                                                                                                                                                                                     -IDKLLSPKNLLITPKDALGRVLQNLTTVAANHGY----TKFSKLIQDSGLLSVITDSI 637
                                                                                                                                                                                                                                                                                  LKVTTSATT--LQGEPVSISVS--QDTVFINNEAKVLSSDIIS-----TNGVIHV 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDPDGKASCKCAAGFRGNGTVCTA-INACETSNGGCSTKADCKRTTPGNRVCVCKAGYTG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---ACS---CVH-GRCSQGPLGDGS--CDCDVGWRGVKCDMEITTDNC-NGTCHTSANCL 311
                                    TLQGSELSVRCGTGSDIGELF----LNEQMCRFIHRGLLFDVGVAYGIDCLLMNPTLGGR 753
                                                                                                                    HTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWK 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D------DCSENIDDC-AFASCTPGSTCIDRVASFSCMCPEGKAGLLCHLDDACISN-
                                                                                                                                                                                                                                                IGGFTCLCMPGFKGVHCELEINECQSNPCVNNGQCV---DKVNRFQCLCPPGFTGPVCQI
                                                                                                                                                                                                                                                                                                                            --EHAGKCVNTDGAF------HCECLKGYAGPRCEMDINECHSDPCQNDATCLDK 474
                                                                                                                                                                                                                                                                                                                                                                                                             -PCHKGALCDTNPLNGQYICTCPQGYKGADCTEDVDECAMANS-
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amino acid
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IDLVNGYQCNCQPGTSGVN 641
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                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                             REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/083,590A
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1128
                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
COMPUTER: IF
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: רבווון
מחששבת: 1155 Avenue
                                                                                                TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                            ZTP:
                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
               STRANDEDNESS:
                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
TOPOLOGY:
                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENAAVCKESPNFESYTCLCAPGWQGQ--RCTIDIDEC---ISKPCMNHGLCHNT-QGSYM 896
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GCAKVAKCSQKGTQVSCSCKKGYKGDGYSC-IEIDPCADGVNGGCHEHATCRMTGPGKHK 1015
                                                                                                                                               -----CHTGFNGTACELCWHGRFGPDCQ------PRSCSEHGQCDEGITGSGECLCETG
                                                                                                                                                                                    -----CRKGAT-----CINGVNGFRC-ICPEGPHHP-----SCYSQVNECLSNP
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                                    FKGYNCQ--VNIDECASNPCLNQGTCFDDISGYTCHCVLPYTGK--NCQTVLAPCSPNPC
                                                                       WTAASCDTPTAVFAVCTPACSVHATCTEN - - - NTCVCNLNYEGDGITC - TVVDFCKQNNG
                                                                                                             {\tt CIHGNCTGGLSGYKC-LCDAGWVGINCEVDKNECLSNPCQNGGTCDNLVNGY-RCTCKKG}
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Pred. No. 6.9e-28;
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/01
FILING DATE: 25-UUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,6
                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEPAX: 212 8698864/9741
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TITLE OF INVENTION:
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PRIOR APPLICATION DATA:
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                   169
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                   Local Similarity es 270; Conserv
                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                                                             QKNRCDNNDTIIVRGECGKC----
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                 RKCIYSIYFMGKRSVFIGCQPQCVRTIITRACWLASLAHNAKPAPGEVKMCALGTASVWD
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                                                       EKNRCQNGGTCVAQAMLGKATCRCASGFTGEDCQYSTSHPCFVSRPCLNGGTCHMLSRDT
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                                                                                                                                                                                                                                                                                                                                   2471 amino acids
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                                                                                                                               Score 450.5; DB 3,
Pred. No. 6.9e-28;
Pred. No. 6.9e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version
                                                                                             SQQAPCPLETKPL-----RET 168
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No. 6083904ch
                                                                                                                                                                       Length 2471;
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VHCENNI ---
                                     QKCGANVVGIVDYGSRANKSEMWDVFCYR-----MKDVNCTCKAGYVG
                                                                                                                   LTFDKAK ---
                                                                                                                                                                                           CECKSHYVGDGVDCEPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHLRSPLGQYK 1075
                                                                                                                                                                                                                                                                                                                                                 WTAASCDTPTAVFAVCTPACSVHATCTEN---NTCVCNLNYEGDGITC-TVVDFCKQNNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt RRNVEGCQNLCTVVIQTPRCCHGYFMPDCQACPGGPDTPCNNRGMCRDLYTPMGQCL----}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -IDKLLSPKNLLITPKDALGRVLQNLTTVAANHGY----TKFSKLIQDSGLLSVITDSI 637
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                                                                           FTGDKCQTDMNECLSEPC-KNGGTCSDYVN-SYTCK-----CQAG------
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                                                                                                                                                                                                                                                                                                               FKGYNCQ--VNIDECASNPCLNQGTCFDDISGYTCHCVLPYTGK--NCQTVLAPCSPNPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----QIDECYSSPCLNDGRC-----IDLVNGYQCNCQPGTSGVN
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NECTESSCENGGTCVDGINSFSCLCPVGFTG
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                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 274; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application Patent No. 5869282
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pleming, RAPPLICANT: Artavanis-APPLICANT: Mann, Robe APPLICANT: Gray, Grac TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILIN. LALE CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
NAME: Misrock, S. Leslie
18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 7320
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,159
FILING DATE: 07-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                     403
                                                                                                                                 341
                                                                                                                                                                                                    296 DR----PGECECRPGWRGPLCNECMYYPGCKHGSCNGSA-----WKCVCDTNWG 340
                                                                                                                                                                                                                              271 SQGPLGDGSCDCDVGWRGVKCDMEITTDNC-NGTCHTSANCLLDPDGKASCKCAAGFRGN 329
                                                                                                                                                                                                                                                                                                       237 QCGLGFNGTACET-----CSCVHGRC 270
                                                           397
                                                                                            389 DRNAECTQTGPNQA-----
                                                                                                                                                                   330 GTVCTA-INACETSNGGCSTKADCKRTTPGNRVCVCKAGYTGDGIVCLEINPCLENHGGC 388
                                                                                                                                                                                                                                                                                 236 QCAVTYYNTTCTTFCRPRDDQFGHYACGSEGQKLCLNGWQGVNCEEAICKAGCDPVHGKC
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STATE: New Yor
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                                                   RNGGTCTLKTSNRTQAQVYRTSHGRSNMGRPVRRSSSMRSLDHLRPEGQALNGSSSSGLV 456
                                                                                                                              GILCDQDLNFCGT-HEPCKHGGTCENTAPDKYRCTCAEGLSGEQCEIVE-HPCATR--PC
                 -----VCNCLPKYTGDGKVCSLINVCLTNNGGCSPFAFCNYTEQDQRICT 447
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10036-2711
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Lewis, Julian H.
                                                                                                                                                                                                                                                                                                                                                      5.3%; Score 413.5; DB 2; Length 1404; ilarity 19.7%; Pred. No. 3.4e-25; Conservative 127; Mismatches 482; Indels 507;
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                                                                                                                                                                                                                                                                                                                                                          Indels 507; Gaps
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1319	CONTROL CONTRO	σn υ	Db VY
105	Tana 12050gm/gaboognagoognago 1boo tagoooy 11mgm 124 modelagood		2
1265	KAPPIAATAAHSGLGTGLECAV-VLVUGALALAXSYERKKOKTT	1207	Db Vy
1206		1147	Db
1310	SQLLITESQDQLHQETRFVDGRSILQWDIIAANGILHTISEPL	1268	Qy
1146	CARLTILLALERVGKGASVEGLCSLVRVLLAAQLIKKPASTFGQDPGMLMVLCDLKTGTN	1087	Db
1267		1237	Оу
1086	GVCKQHEVCVPALSETCLSSPCNVRGDCRALEPSRRVAPPRLPAKSSCWPNQAVVNEN	1029	Db
1236		1181	Qy
1028	TEDDENCNACVCENGTSRCTNLWCGLPNCYKVDPLSKSSNLS	987	Db
1180		1121	Qy
986	ICPPGRHGLRCEILLSDPKSACQNASNTISPYTALNRSQNWLDIALTGR-	938	Db
1120	SGRVA	1068	Qy
937	-SGAGWFRCVCAQGFSGPDCRINVNECSPQPCQGGATCIDGIGGYSC	892	Db
1067	GQCHPDASCADLYFQDTTVGVFHL	1008	Оу
891		843	Db
1007	DFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIE-IDPCADGVNGGCHEHATCR	949	Qy
842	-DGDFTCECMSGWTGKRCSERATGCYAGQC	814	Db
948		889	Qy
813	LPCSGHGSCEMSDVGTFCKCHVGHTGTFCEHNLNECSPNPCRNGGICLDG	764	Db
888	GQCLCHTGFNGTACELCWHGRFGPDCQPRSCSEHGQCDEG	831	Qy
763	EQLRPLCSQPPCNEGCFANVSLATSATTTTTTTTTATTTRKMAKPSG	717	Db
830	NPLPFRRNVEGCQNLCTVVIQTPRCCHGYFMPDCQACPGG	791	Оу
716	VGKFNCICPLGYSGSLCEEAKENCTPSPCLEGHCLNTPEGYYCHCPPDRAGKHC	663	Db
790	AYGIDCLLMNPTLGGRCDTFTTFDIPGECGSCIFTPKCPLKSKPKGVKKKCIY	738	Оу
662		639	Db
737	HVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGV	678	Qy
638	RCACASGFTG	625	Db
677	1QDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKF	624	Qy
624	SAVASTSLAIGPCINAKECRNQPGSFACICKEGWGGVTCAENLDDCVGQCRNGATCID-L	566	Db
623	- [-	568	Qy
565	HSAGlaanalltttatataligsnlsStallaalt	533	Db
567	SQDTVFINNEA	508	Оу
532	CPPEWHGDVCQVD	513	Db
507		448	Qy
512	SLGSLQLQQQLAPDFTCDCAAGWTGPTCE-INIDECAGGPCEHGGTCIDLIGGFR-CE	457	Db

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                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-611-729A-2
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US-08-611-729A-2
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1404 amino acids
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               389 DRNAECTOTGPNQA---
                                                     341
                                                                                       330 GTVCTA-INACETSNGGCSTKADCKRTTPGNRVCVCKAGYTGDGIVCLEINPCLENHGGC
                                                                                                                                 296
                                                                                                                                                                 271 SQGPLGDGSCDCDVGWRGVKCDMEITTDNC-NGTCHTSANCLLDPDGKASCKCAAGFRGN 329
                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 06-MAF CLASSIFICATION: 435
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                                                     GILCDQDLNFCGT-HEPCKHGGTCENTAPDKYRCTCAEGLSGEQCEIVE-HPCATR--PC 396
                                                                                                                               DR----PGECECRPGWRGPLCNECMVYPGCKHGSCNGSA-----
                                                                                                                                                                                                       QCAVTYYNTTCTTFCRPRDDQFGHYACGSEGQKLCLNGWQGVNCEEAICKAGCDPVHGKC 295
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Henrique, Domingos M.P.
Lewis, Julian H.
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Artavanis-Tsakonas, Spyridon
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06-MAR-1996
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1207 ETARVADGSGHS-LLIGVLCGVFIVLVGFSVFISLYWKQRLAYRTSSGMNLTPSLDALRH 1265
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- 1354	RAPPTAATAAHSGLGTGIFCAVVLVTGAIALAAYSYFRLKQRTT	1311	Ωу
L 1206	DTVELTVSSSKLNDPQLPVAVGLLGELLSSRQLNGIQRRKELELQHAKLAALTSIVEVKL	1147	Дb
L 1310	SQLLITFSQDQLHQETRFV	1268	Qу
N 1146	CARLTILLALERVGKGASVEGLCSLVRVLLAAQLIKKPASTFGQDPGMLMVLCDLKTGTN	1087	Db
G 1267		1237	Qy
N 1086	GVCKQHEVCVPALSETCLSSPCNVRGDCRALEPSRRVAPPRLPAKSSCWPNQAVVNEN	1029	Db
- 1236	QVLMSEPSLTNELTEVLAFSKSSARGQAFLKHLTDLSIRGTLFVPQNSGLPGNKSL	1181	Qy
s 1028	TEDDENCNACVCENGTSRCTNLWCGLPNCYKVDPLSKSSNLS	987	Db
L 1180	YPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGYVGDGFSCSGNLL	1121	Qу
- 986	IAI	938	Db
A 1120	RSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVA	1068	Qу
C 937	-SGAGWFRCVCAQGFSGPDCRINVNECSPQPCQGGA	892	Db
L 1067	VGDGVDCEP	1008	Qy
E 891	QNGGTCMPGAPDKALQPHCRCAPGWTGLFCAEAIDQCRGQPCHNGGTCE	843	Db
R 1007	DFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSGIE-IDPCADGVNGGCHEHATCR	949	Qy
- 842	-DGDFTCECMSGWTGKRCSERATGCYAGQC	814	Db
V 948	ITGSGECLCETGWTAASCDTPTAVFAVCTPACSVHATCTENNTCVCNLNYEGDGITCTVV	889	Qy
G 813	LPCSGHGSCEMSDVGTFCKCHVGHTGTFCEHNLNECSPNPCRNGGICLDG	764	Db
G 888	YTPMGQCLCHTGFNGTACELCWHGRFGPDCQPRSCSEHGQCD	831	Qy
G 763	EQLRPLCSQPPCNEGCFANVSLATSATTTTTTTTTTTTTKMAKPSG	717	Db
G 830	NPLPFRRNVEGCQNLCTVVIQTPRCCHGYFMPDCQACPGG	791	Qy
- 716	VGKFNCICPLGYSGSLCEEAKENCTPSPCLEGHCLNTPEGYYCHCPPDRAGKHC	663	DЪ
Y 790	GSCIFTP	738	Qy
м 662	RDCETDIDECATSPCRNGGECCDM	639	Db
V 737	HVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGV	678	Qy
- 638	VNDYRCACASGFTG	625	Db
F 677	IQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKF	624	Qy
L 624	SAVASTSLAIGPCINAKECRNQPGSFACICKEGWGGVTCAENLDDCVGQCRNGATCID-L	566	рb
L 623	KVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKL	568	Qy
T 565	HSAGIAANALLTTTATATIGSNLSSTALLAALT	533	Дb
A 567	ATTLOGEP	508	Qy
- 532	CPPEWHGDVCQVDVNECEAP	513	Db
E 507	CKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHE	448	Qy
E 512	SLGSLQLQQQLAPDFTCDCAAGWTGPTCE-INIDECAGGPCEHGGTCIDLIGGFR-CE	457	Db
r 447	VCNCLPKYTGDGKVCSLINVCLTNNGGCSPFAFCNYTEQDQRICT	403	Qy

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                                                                                                                                                                                    Query Match
Best Local Similarity 22.0
Matches 231; Conservative
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,159
FILING DATE: 07-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1193 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION:
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309 NCLLDPDGKASCKCAAGFRGNGTVC-TAINACETS---NGGCSTKADCKRTTPGNRVCVC
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                   POCVRTIITRACWLASLAHNAKPAPGEVKMCALGTASVWDGVNGTGTCQCGLGFNGTACE
                                                                                    TCTEGKYGIHCDQACSCVHGRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNCNGTCHTSA
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                                                                                                                   New York
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(212) 869-9741/8864
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Gray, Grace E.
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Myat, Anna M.
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22.0%; Pred. No. 5.1e-25;
ative 72; Mismatches 323;
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RESULT 12
US-08-611-729A-10
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                                                                                                    DKAKEACAKEAATIATYNQLSYAQKAKYHLCS 1110
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                                                                                                                                                                    -GQCHPD-----ASC-ADLYFQDTTVGVFHLRSPLGQYKLTF 1078
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Sequence 10, Application US/08611729A Patent No. 6004924

GENERAL INFORMATION: APPLICANT: Ish-Ho

APPLICANT: APPLICANT: APPLICANT:

Lewis, Ju Myat, Ann Fleming, Henrique, Ish-Horowicz,

s, Julian H. , Anna M. ing, Robert J. Domingos

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INFORMATION FOR SEQ ID NO: 10:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAL PLOASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,729A
FILING DATE: OG-MAR-1996
CLASSIFICATION: 435
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NAME: MISTOCK, S. Leslie
REGISTRAFION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-037
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MEDIUM TYPE: Floppy disk
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APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
567 AKVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQD 626
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CITY: New York
STATE: New Yor
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                                                                                                        EPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNE 566
                                                                                                                                                                                            TCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNH 506
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                                                                                                                                                    ICSPGYAGDH---CEKDI-NECASNPCMN------GGHCQDEING---FQCLCPAGFSGN- 494
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                                                                NUCLEOTIDE AND PROTEIN SEQUENCES OF THE SERRATE GENE AND METHODS BASED THEREON: 20
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	US-08-882-046-7 US-08-882-046-7 Sequence 7, Application US/08882046 Patent No. 6136952 GENERAL INFORMATION: APPLICANT: Li, Linheng APPLICANT: Hood, Leroy APPLICANT: Krantz, Ian D. APPLICANT: Warning B. TITLE OF INVENTION: Human Jagged Polypeptide, Encoding TITLE OF INVENTION: Nucleic Acids and Methods of Use NUMBER OF SEQUENCES: 110 CORRESPONDENCE ADDRESS: ADDRESSEE: Campbell & Flores LLP STREET: 4370 La Jolla Village Drive, Suite 700 CITY: San Diego STATE: California COUNTRY: USA ZIP: 92122 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRUM APPLICATION NUMBER: US/08/882,046 FILING DATE: 25-JUN-1997 CLASSIFICATION: 536 ATTORNEY/ACENT INFORMATION: NAME: Campbell, Cathryn A.	
	Db 939 TFNKEMMAPGLTTEHICS 956	-
	Qy 1079 DKAKEACAKEAATIATYNQLSYAQKAKYHLCS 1110	_
1078 938	Qy 1030 EPEQLPLDRCLQDNGQCHPDASC-ADLYFQDTTVGVFHLRSPLGQYKLTF	п О
892	Db 834 GRPCFTSIRVMPDGAKWDDDCNTCQCLN-GKVTCSKVWCGPRPCIIHAKGHNECPAGHAC	_
1029	RMTGPGKHKCECKSHYVGDGVDC	^
100 4 833	Qy 973CSCKKGYKG	п О
972 777	Qy 920 CSVHATCTENNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVS Db 727 CHNGGTCVVSGDSFTCVCKEGWEGPTCTQNTNDCSP-HPCYNSGTCVDGDNW	
	676 CHSR-DSQCDEATCNNGGTCYDEGDTFKCMCPAGWEGATCNIARNSSCLPNP	-
919	Qy 862 CELCWHGRFGPDCQPRSCSEHGQC-DEGITGSGECLCETGWTAASCDTPTAVFAVCTP-A	_
861 675	QY 806 CTVVIQTPRCCHGYFMPDCQACPGGPDTPCNNRGMCRDLYTPMGQCLCHTGENGTA Db 629CSDGWEGTYCETNINDCSKNPCHNGGTCRDLVNDF-FCECKNGWKGKT	- 0
2	10 NPCKNGGTCIDGVNSYKCI	п
805	Qy 747 NPTLGGRCDTFTTFDIPGECGSCIFTPKCPLKSKPKGVKK-KCIYNPLPFRRNVEGCQNL	0
609	576HGKCKSQAGGKFTCECNKGFTGTYCHENINDC-ES	п
746	Qy 687 ASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGVAYGIDCLLM	_
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: P-UW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS: LENGTH: 1010 amino acids
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                                                                                                                                                                                                                                                                                         DFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFL
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KCMCPGGWEGTTCN--IARNSSCLPNPCHNGGTCVVNGESFTCVCKEGWEG------P
                          ECLCETGWTAASCDTPTAVFAVCTP-ACSVHATCTENN---TCVCNLNYEGDGITCTVVD
                                                            CHNGGTCRDLVNDF-YCDCKNGWKGKTC----HSR-DSQCDEATCNNGGTCYDEG--DAF
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                                                                                                                              --DGVNSYKCI---
                                                                                                                                                         KPKGVKK-KCIYNPLPFRRNVEGCQNLCTVVIQTPRCCHGYFMPDCQA----CPGGPDTP
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Pred. No. 2.9e-24;
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SEQ ID NO 6
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SAKANO, SEIJI
APPLICANT: ITOH, AKIRA
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE
FILE REFERENCE: KP-8447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 4 SOFTWARE: PatentIn Ver.
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les 229; Conserv
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                                                                                ICTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSF
                                                                                                                         -----NAKSCKNLIASYYCDCLPGWMGQN--CDININDCL---GQCQNDASCRDLVNGYR 441
                                                                                                                                                                 GGCDRNAECTQTGPNQAVCNCLPKYTGDGKVCSL-INVCLTNNGGCSPFAFCNYTEQDQR
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-RIKDW-----DQQGLMSQVLRYHVVGCQQLLLDNLK 539
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N	9CLQDNGQCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAK 108:	Qy 103 Db 86	
ω.	4DGVNG-GCHEHATCR-MTGPGKHKCECKSHYVGDGVDCEPEQLPLDR 1038	Oy 994 Db 804	
	0 FCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIEIDPCA 993	Qy 950 Db 747	
	4 ECLCETGWTAASCDTPTAVFAVCTP-ACSVHATCTENNTCVCNLNYEGDGITCTVVD 949 : :	Qy 894 Db 697	
	5 CNNRGMCRDLYTPMGQCLCHTGFNGTACELCWHGRFGPDCQPRSCSEHGQC-DEGITGSG 893	Qy 835 Db 645	
	0 KPKGVKK-KCIYNPLPFRRNVEGCQNLCTVVIQTPRCCHGYFMPDCQACPGGPDTP 834	Qy 780 Db 615	
	0 NEOMCRFIHRGLLFDVGVAYGIDCLLMNPTLGGRCDTFTTFDIPGECGSCIFTPKCPLKS 779	Qy 720 Db 592	
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	8 -TTPCEVIDSCTVAMA-SNDT	Db 538	
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	NHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLK 5	QY 505	
	15 ICTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSF 504	Qy 445 Db 442	
	GGCDRNAECTOTGPNQAVCNCLPKYTGDGKVCSL-INVCLTNNGGCSPFAFCNYTEQDQR	Qy 386 Db 392	
	1 TVCTAINACETSNGGCSTKADCKRTTPGNRVCVCKAGYTGDGIVCLEINPCLENH 385	Qy 331 Db 339	
•	TCHTSADGKAS	Qy 303 Db 280	
	9 TCTEGKYGIHCDQACSCVHGRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNCNG 302	Qy 249 Db 233	
	9 POCVRTIITRACWLASLAHNAKPAPGEVKMCALGTASVWDGVNGTGTCQCGLGENGTACE 248	Qy 189	
68;	/ Match Local Similarity 21.7%; Pred. No. 3.8e-24; Less 229; Conservative 74; Mismatches 318; Indels 435; Gaps	Query Ma Best Loo Matches	

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Result
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'/cgn2_6/ptcdata/2/paa/US083_COMB.pep:*
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Copyright (c) 1993 - 2000 Compugen
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                Sequence 2, Appli
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Sequence 62, Appl
Sequence 25, Appl
Sequence 21388, Ap
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ALIGNMENTS

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; TYPE: PRT ; ORGANISM: Rattus norvegicus PCT-US01-13403-2
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                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1431
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   Matches 1431;
                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                         FILE REFERENCE: 618754/JP/199,538
CURRENT APPLICATION NUMBER: PCT/US01/13403
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/245,320
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: 60/199,538
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WEIGEL, PAUL H.
APPLICANT: ZHOU, BIN
APPLICANT: WEIGEL, JANET A.
TITLE OF INVENTION: IDENTIFICATION AND USES
                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-04-25
   Conservative
                   100.0%;
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Pred. No. 0;
Mismatches
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                                                                                                                                    WTAASCDTPTAVEAVCTPACSVHATCTENNTCVCNLNYEGDGITCTVVDFCKQNNGGCAK
                                                                                                                                                                                 CRDLYTPMGQCLCHTGFNGTACELCWHGRFGPDCQPRSCSEHGQCDEGITGSGECLCETG
                                                                                                                                                                                             CRDLYTPMGQCLCHTGFNGTACELCWHGRFGPDCQPRSCSEHGQCDEGITGSGECLCETG
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          AKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYASQKCGANVVGIVDY
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AKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYASQKCGANVVGIVDY
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CORRENT APPLICATION NUMBER: US/09/842,930A
CURRENT FILING DATE: 2001-04-22
PRIOR APPLICATION NUMBER: 60/245,320
PRIOR ETLING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: 60/199,538
PRIOR ETLING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 1431
TYPE: PRT
ORGANISM: Rattus norvegicus
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Best Local Similarity
Matches 1431; Conser
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                             NGTCHTSANCLLDPDGKASCKCAAGFRGNGTVCTAINACETSNGGCSTKADCKRTTPGNR
                                                                                                                                                                                                                           GVIHGLEKVLEIQKNRCDNNDTIIVRGECGKCSQQAPCPLETKPLRETRKCIYSIYFMGK 180
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 VCVCKAGYTGDGIVCLEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKYTGDGKVCSLI
                                                                                          GFNGTACETCTEGKYGIHCDQACSCVHGRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNC
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                                                HSGLGTGIFCAVVLVTGAIALAAYSYFRLKQRTTGFQRFDQKRTLMSWLLASSSPRISQT
                                                                                                                  KSSARGQAFLKHLTDLSIRGTLFVPQNSGLPGNKSLSGRDIEHHLTNVNVSFYNDLVNGT
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                                     HSGLGTGIFCAVVLVTGAIALAAYSYFRLKQRTTGFQRFDQKRTLMSWLLASSSPRISQT
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Sequence 25, Appl;
GENERAL INFORMAT

APPLICANT: WEIGI
APPLICANT: WEIGI
APPLICANT: WEIGI
FILE OF INVENT
CURRENT APPLICAT;
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PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: 60/199,538
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 1394
TYPE: PRT
ORGANISM: Home sapiens
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APPLICANT: ZHOU, BIM
APPLICANT: WEIGEL, JANET A.
TITLE OF INVENTION: IDENTIFICATION AND USES
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CURRENT APPLICATION NUMBER: PCT/US01/13403
CURRENT FILING DATE: 2001-04-25
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                                                                         KLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIR
                                                                                                                       YINNKAKIISSDIISTNGIVHIIDKLLSPKNLLITPKDNSGRILQNLTTLATNNGYIKFS
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: GENERAL INFORMATION:
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ORGANISM: Homo sapiens
PCT-US01-13403-62
                                                         SEQ
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TITLE OF INVENTION: IDENTIFICATION AND USES
FILE REFERENCE: 618754/JP/199,538

CURRENT APPLICATION NUMBER: PCT/US01/13403

CURRENT FILING DATE: 2001-04-25
                                                                   PRIOR APPLICATION NUMBER: 60/245,320 PRIOR FILING DATE: 2000-11-02 PRIOR APPLICATION NUMBER: 60/199,538 PRIOR FILING DATE: 2000-04-25 NUMBER OF SEQ ID NOS: 64 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                  APPLICANT: WEIGEL, PAUL H. APPLICANT: ZHOU, BIN
                            TYPE: PRT
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LENGTH: 1192
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PRIOR FILING DATE: 2000-04-25
NUMBER OF SEO ID NOS: 56
SOFTWARE: PatentIn version 3.1
SEO ID NO 25
LENGTH: 1394
TYPE: PRT
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nes 951; Conserv
                                FFYNDLVNGTTLQTRLGSKLLITASQDPLQPTETRFVDGRAILQWDIFASNGIIHVISRP
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VFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSIS
                                                    CNYTEQDQRICTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFT
                                                                                                                     LEINPCLENHGGCDRNAECTOTGPNQAVCNCLPKYTGDGKVCSLINVCLTNNGGCSPFAF
                                                                                                                                                                                        GKASCKCAAGFRGNGTVCTAINACETSNGGCSTKADCKRTTPGNRVCVCKAGYTGDGIVC
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                                                                                                     LEINPCLENHGGCDKNAECTQTGPNQAACNCLPAYTGDGKVCTLINVCLTKNGGCSEFAI
                                                                                                                                                                       -----VCAAGFQGNGTICTAINACEISNGGCSAKADCKRTTPGRRVCTCKAGYTGDGIVC
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                                                                                                                                                                                                                                                                                                                                             ITRACWLASLAHNAKPAPGEVKMCALGTASVWDGVNGTGTCQCGLGFNGTACETCTEGKY
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US-60-230-445-1388; Sequence 1388; Appli; GENERAL INFORMATION:

Application US/60230445

APPLICANT: Beasley, Ellen TITLE OF INVENTION: ISOLA: TITLE OF INVENTION: AND USE TITLE REFERENCE: CL000765

ISOLATED HUMAN TRANSPORTER PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN AND USES THEREOF

TRANSPORTER PROTEINS

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                                                                                                                                      QDQLH-QETRFVDGRSILQWDIIAANGILHIISEPLRAPPTAATAAHSGLGTGIFCAVVL 1334
                                                                                                                                                                                                     LSIRGTLEVPQNSGLPGNKSLSGRDIEHHLTNVNVSFYNDLVNGTFLRTMLGSQLLITTFS 1275
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                                                                                                                         QDPLQPTETRFVDGRAILQWDIFASNGIIHVISRPLKAPPAPVTLTHTGLGAGIFFAIIL 1313
                                                                                                                                                                                      LSIRGTLFVPQNSGLGENETLSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGSKLLITAS 1253
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-PSYDPFTDSE
                           HPQSPPVTPSQ 1399
                                                           VTGAVALAAYSYFRINRRTIGFQHFESEEDINVAALGKQQPENISNPLYESTTSAPPE--
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; ORGANISM: HUMAN
US-60-230-445-1388
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CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 3051
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1388
LENGTH: 1895
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Best Local
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                                                                                                                                                                                            FHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVG 736
                                                                                                                                                                                                                                       YIKFSNLIQDSGLLSVITDPIHTPVTLFWPTDQALHALPAEQQDFLFNQDNKDKLKEYLK
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                                                                                                                              VAYGIDCLLMNPTLGGRCDTFTTFDIPGECGSCIFTPKCPLKSKPKGVKKKCIYNPLPFR 796
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                                              RNVEGCQNLCTVVIQTPRCCHGYFMPDCQACPGGPDTPCNNRGMCRDLYTPMGQCLCHTG 856
                                                                                                                                                                               FHVIRDAKVLAVDLPTSTAWKTLQGSELSVKCGAGRDIGDLFLNGQTCRIVQRELLFDLG
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               FNGTACELCWHGRFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVC
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Sequence 63, Application PC/TUS0113403
GENERAL INFORMATION:
APPLICANT: WEIGEL, PAUL H.
APPLICANT: ZHOU, BIN
APPLICANT: WEIGEL, JANET A.
APPLICANT: WEIGEL, JANET A.
TITLE OF INVENTION: IDENTIFICATION AND USES OF
FILE REFERENCE: 618754/JP/199,538
CURRENT APPLICATION NUMBER: PCT/US01/13403
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/243,320
PRIOR APPLICATION NUMBER: 60/199,538
PRIOR FILING DATE: 2000-01-02
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 64
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                                                                                                  NOLSYAQKAKYHLCSAGWLESGRVAYPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCY 1155
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                        HPQSPPVTPSQ
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                                                 VTGAVALAAYSYFRINRRTIGFQHFESEEDINVAALGKQQPENISNPLYESTTSAPPE--
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TITLE OF INVENTION: IDENTIFICATION AND USES OF A HYALURONAN RECEPTOR FILE REFERENCE: 618754/JP/199,538
CURRENT APPLICATION NUMBER: PCT/USO1/13403
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/245,320
PRIOR FILING DATE: 2000-01-02
PRIOR FILING DATE: 2000-01-02
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 64
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EGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIEIDPCADGVNG
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                                                                            VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTCKVGYVGDGFSCSGN
                                                                                           VAYPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGYVGDGFSCSGN 1178
                                                                                                                                                  DTTYGYFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYAQKAKYHLCSAGWLETGR
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
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Best Local 9
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EARLIER FILING DATE: 198-12-23
NUMBER OF SEO ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
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 SLRLLEYKELKGDGPFTIFVPHADLMSNLSQDELARIRAHRQ-----LVFRYHVVGCRRL 1240
                                    QLQEHAVRELAGPGPFTVFAP---LSSSFNHE--PRIKDWDQQGLMSQVLRYHVVGCQQL
                                                                        TCTCQDGYMGDGELCQEINSCLIHHGGCHIHAECIPTGPQQVSCSCREGYSGDGIRTCEL
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US-09-466-778-2

Sequence 2, Application US/09466778 GENERAL INFORMATION:

APPLICANT: Hastings, Gregg TITLE OF INVENTION: NOVEL FILE REFERENCE: PF487

Hyaluronan-Binding

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CURRENT APPLICATION NUMBER: US/09/466,778
CURRENT FILING DATE: 1999-12-20
EARLIER APPLICATION NUMBER: 60/113,871
EARLIER FILING DATE: 1998-12-23

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                                                                   PGTVVVSRIIVWDIMAFNGIIHALASPLLAPPQPQAVLAXEAPPVAAGVGAVLAAGALLG
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                                                                                                                                    NEGFVDNMTLSGPNLELHASNATLLSAN-ASQGKLLPAHSGLSLIISDAGPDNSSWAPVA
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NUMBER OF SEQ ID NOS: 37 SOFTWARE: PatentIn Ver. 2.0

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-466-778-2
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                                                                                                                                                                                                                             LPPDRQAWLYHEDHRDKLAATLRGHMIRNVEALASDLPNLGPLRTMHGTPISFSC-SRTR 1419
                                                                                                                                                                                                                                                                                                                                                                                                           LLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNL 593
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                                                                                                                                                                                         IGELFLNEOMCRFIHRGLLFDVGVAYGIDCLLMNPTLGGRCDTFTTFDIP-GECGSCIFT 772
                                                                                                                                                                                                                                                                                                                                    LITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEA 653
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                                                                        {\tt PPCPEGSQEQGSPEACWRFYPKFWTSPPLHSLGLRSVWVHPSLWGRPQGLGRGCHRNCVT}
                                                                                                              PKCPLKSKPKGVKKKC-----IYNPLPFR----RNV-----
                                                                                                                                                   PGELMVGEDDARIVQRHLPFEGGLAYGIDQLLEPPGLGARCDHFETRPLRLNTCSICGLE 1479
                                                                                                                                                                                                                                                                  LPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSD 713
                                                                                                                                                                                                                                                                                                          LHWEPDDAPIPRRNVTAAAQGFGYKIFSGLLKVAGLLPLLREASHRPFTMLWPTDAAFRA 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDPCSKNNGGCSPYATCKSTGDGQRTCTCDTAHTVGDGLTCRARVGLELLRDKHAS--FF 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFHGTACEVCELGRYGPNCTGVCDCAHGLCQEGLQGDGSCVCNVGWQGLRCDQKITSPQC
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; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 60
                                                                                                                                                                  Matches
                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: WEIGEL, JANET A.

TITLE OF INVENTION: IDENTIFICATION AND USES OF A HYALURONAN RECEPTOR FILE REFERENCE: 618754/JP/199,538

CURRENT APPLICATION NUMBER: PCT/USO1/13403

CURRENT FILING DATE: 2001-04-25

PRIOR APPLICATION NUMBER: 60/245,320

PRIOR APPLICATION NUMBER: 60/245,320

PRIOR PILING DATE: 2000-11-02

PRIOR PILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-04-25
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                                      RYHVVLGEKLLKNDLHNGMHRETMLGFSYLLAFFLRNDQLYVNEAPINYTNVATDKGVIH 124
                                                                                   LLQQLDLVPAFSLFRELLQHHGLVPQIEAATAYTIFVPTNRSLE-
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                                                                                                                                                               Conservative 222; Mismatches 546;
                                                                                                                                                                                 35.7%; Score 2810; DB 1; 40.0%; Pred. No. 7.5e-199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFGPHCQACRCTVHGRCDEGLGGSGSCFCDEGWTGPRCEVQLELQPVCTPPCAPEAVCRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLRLLEYKELKGDGPFTIFVPHADLMSNLSQDELARIRAHRQ-----LVFRYHVVGCRRL
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                                                                                                                                                         SDAMCTDQHFQEKRAGVFHLQATSGPYGLNFSEAEAACEAQGAVLASFPQLSAAQQLGFH
                                                                                                                                                                                                                                                                                             IDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDC-EPEQLPLDRCLQDNGQCH 1047
                                                                                                                                                                                                                                                                                                                                                                    GNSCECSLGYEGDGRVCTVADLCQDGHGGCSEHANCSQVGTMVTCTCLPDYEGDGWSCRA 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVHATCTE 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \verb|TTWKPSCCPGHYGSECQACPGGPSSPCSDRGVCMDGMSGSGQCLCRSGFAGTACELCAPG|
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YVGDGFS-CSGNLLQVLMSFPSLTNFLTEVLAFSKSSARGQAFLKHLTDLSIRGTLFVPQ 1226
                                                                                                  LCSAGWLESGRVAYPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAG
                                                                                                                                                                                                           PDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYH 1107
                                                                                                                                                                                                                                                               RNPCTDGHRGGCSEHANCLSTGLNTRRCECHAGYVGDGLQCLEESEPPVDRCLGQPPPCH 1082
                                                                                                                                                                                                                                                                                                                                                                                                                      NNTCYCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIE 988
                                                      LCLMGWLANGSTAHPVVFPVADCGNGRVGVVSLGARKNLSERWDAYCFRVQDVACRCRNG
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RESULT 12
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LENGTH: 1458
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Matches 560;
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APPLICANT: WEIGEL, JANET A.
APPLICANT: WEIGEL, JANET A.
TITLE OF INVENTION: IDENTIFICATION AND USES OF A HYALURONAN RECEPTOR
FILE REFERENCE: 618754/JP/199,538
CURRENT APPLICATION NUMBER: PCT/US01/13403
CURRENT FILING DATE: 2001-04-25
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PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: 60/199,538
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
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  INVCLTNNGGCSPFAFCNYTEQDQRICTCKPDYT-GDGIVCRGSIYGELPKNPSTSQYFF
                                                                                                                                                NGTCHTSANCLLDPDGKASCKCAAGFRGNGTVCTAINACETSNGGCSTKADCKRTTPGNR
                                                                                                                                                                                                                      GFNGTACETCTEGKYGIHCDQACSCVHGRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLTRLEQMPDYSIFRGYIIHYNLASAIESADAYTVFVPNNEAIENYIREKKATSLKEDIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RYHVVLGEKLLKNDLHNGMHRETMLGFSYLLAFFLRNDQLYVNEAPINYTNVATDKGVIH 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLQQLD-LVAFSLFRELLQHHGLVPQIEAATAYTIFVPTNRSLE----AQGNSSHLDADTV
                                                                          VCVCKAGYTGDGIVCLEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKYTGDG-KVCSL 419
                                                                                                                                                                                                   GFHGTACEVCELGRYGPNCTGVCDCAHGLCQEGLQGDGSCVCNVGWQGLRCDQKITSPQC
                                                                                                                                                                                                                                                                               R----GCSYTCAKKIOVPDCCPGFFGTLCEPCPGGLGGVCSGHGQCQDRFLGSGECHCHE 249
                                                                                                                                                                                                                                                                                                                                                         GLSGYLTYGSSRCLHSHAEALREKCYNCTRRFRCTQGFQLQDTP---RKSCYYRSGFSFS 193
                                       TCTCQDGYMGDGELCQEINSCLIHHGGCHIHAECIPTGPQQVSCSCREGYSGDGIRTCEL
                                                                                                                     PRKCDPNANCVQDSAGASTCACAAGYSGNGIFCSEVDPCAHGHGGCSPHANCTKVAPGQR
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40.0%; Pred. No. 7e-
tive 220; Mismatches
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ACIDS ENCODING

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RESULT 13
US-09-715-417A-16
; Sequence 16, Application US/09715417A
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                    DG-----RSILQWDIIAANGILHIISEPLRAPPTAATAAHS----GLGTGIFCAVVLVTGA
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PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 60/187,844
PRIOR FILING DATE: 2000-03-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
SEO ID NO 16
RESULT 14
US-09-715-417A-12
Sequence 12, Application US/09715417A
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard
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Best Local Similarity 78.8
Matches 471; Conservative
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CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/166,336
PRIOR FILING DATE: 1999-11-19
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APPLICANT: Shimkets,

Richard

Lichenstein,

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US-09-715-417A-12
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CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/165,336
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 60/167,785
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 60/187,844
PRIOR APPLICATION NUMBER: 60/187,844
PRIOR FILING DATE: 2000-03-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
Sequence 2725, Application PC/TUS0116450 GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Nucleic Acids, Prot
FILE REFERENCE: PA131PCT
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Best Local
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APPLICANT:
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                                                                                                                                                                                                NNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIE
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Fernandes,
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PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2820
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2725
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Best Local Similarity
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GSTAHPVVFPVADCGNGRVGIVSLGARKNLSERWDAYCFRVQDVACRCRNGFVGDGISTC
                GRVAYPTTYASOKCGANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGYVGDGFS-C
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PCT-US02-09671-703
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Sequence 37, Appl	6 US-10-123-155-37	ī	350	3.6	284.5	45
Sequence 6445, Ap	7 US-60-360-039-6445	à	838	3.6	286.5	44
Sequence 6816, Ap	7 US-60-360-039-6816	7	1557	3.7	288.5	3
Sequence 38, App	6 US-10-121-062-38	7	737	3.7	289.5	42
Sequence 5166, Ap	7 US-60-360-039-5166	4	282	3.7	292	41
Sequence 31, Appl	5 US-09-970-944-31	نت	153	3.7	292	40
Sequence 52, App.	6 US-10-042-865-52	'n	271	3.7	294	39
Sequence 5821, Ap	7 US-60-360-039-5821	ű	129	3.8	295	38
Sequence 5820, Ap	7 US-60-360-039-5820	ű	1295	3.8	295	37
Sequence 30, App	5 US-09-970-944-30	4	153	3.8	295.5	36
Sequence 6539, Ap	7 US-60-360-039-6539	ت	387	3.8	297	35
Sequence 6538, Ap	7 US-60-360-039-6538	تر	387	3.8	297	34
Sequence 2,	7 US-60-369-876-2	ã	98	3.8	299	w
Sequence 396, App	5 US-09-312-283B-396	ő	1529	3.9	306	32
Sequence 527	7 US-60-360-039-5221	ũ	2823	3.9	307	31
Sequence 5220, Ap	7 US-60-360-039-5220	ũ	2823	3.9	307	30
Sequence 32, Appl	5 US-09-970-944-32	2	151	4.0	312.5	29
Sequence 216, App	1 PCT-US02-08253-216	7	1247	4.0	315.5	28
sequence 29,	67-8TTG-99/-60-SN C	ú	SZCT	4.	27.0	-

ALIGNMENTS

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; ORGANISM: homo sapiens US-10-123-962-2
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 2
LENGTH: 1986
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Best Local Similarity 77.0
Matches 1083; Conservative
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APPLICANT: Zambrowicz, Brian
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871 CNGTCHTSANCLTNSDGTASCKCAAGFQGNGTICTAINACEISNGGCSAKADCKRTTPGR
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                                                   SNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLANVSMFFYNDLVNG
                                                                                                                                   SKSSARGQAFLKHLTDLSIRGTLFVPQNSGLPGNKSLSGRDIEHHLTNVNVSFYNDLVNG
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 SNPLYESTTSAPPE --- PSYDPFTDSE
                    SSPRISQTLCMRPQRRHPQSPPVTPSQ
                                         LTHTGLGAGIFFAIILVTGAVALAAYSYFRINRRTIGFQHFESEEDINVAALGKQQPENI
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APPLICANT: Gerhardt, Brenda
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: Novel Human EGF-Family F
FILE REFERENCE: LEX-0338-USA
CURRENT APPLICATION NUMBER: US/10/123,962
CURRENT FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/286,141
PRIOR FILING DATE: 2001-04-24
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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 DFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFL
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RESULT 3
US-10-104-047-2580
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APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: NOVEL full length FILE REFERENCE: H1-A0105
                                                                                                                                                                               NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 2580
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/104,047 CURRENT FILING DATE: 2002-03-25 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                    ORGANISM: Homo
                                                                                                                                      TYPE: PRT
                                                                                                                                                         LENGTH: 510
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PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3794, Application US/10104047 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/104,047 CURRENT FILING DATE: 2002-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 482
                     1209
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FLKHLTDLSIRGTLFVPQNSGLPGNKSLSGRDIEHHLTNVNVSFYNDLVNGTFLRTMLGS 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDFLDFLDDELTYKTLFVPVNEGFVDNMTLSGPDLELHASNATL
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                                                                                                                                                        ATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYASQKCGANVVGIVDYGSRANKSEM 1149
                                                                                                                                                                                                                                                                                    VTCTCLPDYEGDGWSCRARNPCTDGHRGGCSEHANCLSTGLNTRRCECHAGYVGDGLQCL
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                                                          WDAYCFRVQDVACRCRNGFVGDGISTCNGKLLDVLAATANFSTFYGMLLGYANATQRGLD
                                                                                             WDVFCYRMKDVNCTCKAGYVGDGFS-CSGNLLQVLMSFPSLTNFLTEVLAFSKSSARGQA 1208
                                                                                                                                  AVLASFPQLSAAQQLGFHLCLMGWLANGSTAHPVVFPVADCGNGRVGVVSLGARKNLSER\\
                                                                                                                                                                                                          EESEPPVDRCLGQPPPCHSDAMCTDLHFQEKRAGVFHLQATSGSYGLNFSEAEAACEAQG
                                                                                                                                                                                                                                             EPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEA 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERWDAYCFRVQDVACRCRNGFVGDGISTCNGKLLDVLAATANFSTFYGMLLGYANATQRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGAVLASFPQLSAAQQLGFHLCLMGWLANGSTAHPVVFPVADCGNGRVGVVSLGARKNLS
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Pred. No. 2.3e-35;
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Qy 437 NYTEODQRICTCKPDYTGDGIVCRGSIYGELPKNPS ::	Oy 385 HGG-CDRNAECTQTGPNQAVCNCLPKYTGDGKVCSLINVCLTNNGG-	OY 345GCSTKADCKRTTPGNRVCVCKAGYTGDGIVCLEINPCLEN	Qy 312 LDPDGKASCKCAAGFRGNGTVCTAINACETSNG 1:	Qy 266 VH-GRCSQGPLGDGSCDCDVGWRGVKCDMEIT : : :: :	Qy 221LGTASVWDGVNGTGTCQCGLGFNGTACE-TCTEGKYGIHCDQACSC	Qy 164 PLRETRKCIYŞIYFMGKRSVFIGCQPQCVRTIITRACWI : ::	Qy 115 NVATDKGVIHGLEKVLEIQKNRCDNNDTIIVRGECGKCSQQAPCP :	Query Match 6.1%; Score 480.5; DB Best Local Similarity 22.2%; Pred. No. 3.1e-19 Matches 251; Conservative 98; Mismatches 34	RESULT 5 US-60-360-039-5280 Sequence 5280, Application US/60360039 GENERAL INFORMATION: APPLICANT: Chen, Xianfeng APPLICANT: Chen, Xianfeng APPLICANT: GOLdman, Barry J. APPLICANT: Hinkle, Gregory J. APPLICANT: Slater, Steven C. TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTITITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTITILE OF INVENTION: DIANTS WITH IMPROVED PROPER FILE REFERENCE: 38-10(52052)A CURRENT FILLING DATE: 2002-02-21 UMBER OF SED ID NOS: 47374 SEQ ID NO 5280 LENGTH: 1111 TYPE: PRT ORGANISM: Caenorhabditis elegans US-60-360-039-5280	Oy 1352 RTTGF 1356 Db 416 KPTGF 420	Qy 1299 ANGILHIISEPLRAPPTAATAAHSGLGTGIFCAVVLVTGAI- : ::	
IVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGP 491	CSLINVCLTNNGGCSPFAFC 436	NRVCVCKAGYTGDGIVCLEINPCLEN 384 ::	CTAINACETSNG 344 : :: : CDCLNNQNCDSSSGECKCIGWTGKHC 317	-GVKCDMEITTDNCNGTCHTSANCL 311 : :	GTCOCGLGFNGTACE-TCTEGKYGIHCDQACSC 265	-RTIITRACWLASLAHNAKPAPGEVKMCA- 220 :	NDTIIVRGECGKCSQQAPCPLETK 163 	BB 7; Length 1111; 19; 341; Indels 441; Gaps 70;	PROTEINS IN PLANTS FOR PRODUCTION OF		VVLVTGAIALAAYSYFRLKQ 1351 : : avlaagallglvagalylrarg 415	SLIISDAGPDNSSWAPVVSLATVPPCWPWPSLTVGLTLVSLQAPGTVVVSR-IIVWDIMA 359

Oy 134 KNRCDNNDTIIVRGECGKCSOOAPCDLET-KPLRETRKCIYSIYFMGKRSVFIGCQP--Q 190 | | | | | : : | : : | ::| : | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | | ::|: | | | ::|: | | | ::|: | | | ::|: | | | ::|: | | | ::|: | | | ::|: | | | ::|: | | | ::|: | | | ::|: | | | ::|: | | | ::|: | | | ::|: | | | ::|: | | | ::|: | | | ::|: | | ::|: | | ::|: | | ::|: | | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|: | ::|:

2571	LOEF	2TC2	ΩÜ
1		л З	7
562	DKALEALPPEQQDFL 6	648	Qγ
2511	LSESSTTPESSSKSPVSSSTEGISVVTSTEFSK-VPESTISSVLEEDLTKTTPSPILEET 2	2453	Db
547	: : : : LLSVITDSIHTPVT	616	Oy
2452	NIPEASSKQTISSTPT	2393	Db
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1 1	7007 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	n o	?
2392	TEAPTTLSPDILSTTTNNLSQSSTVSTEDRSEISSENSEKPTSAPELVTSSVTHVASSSP	2333	Db
588		573	Qy
2332	TPMNSNSEVLTTSEPHVLSSSLSPDVSQSSTTPNNLSESSTVETPKTSSEVSLNSEEPST 2	2273	Db
572		553	Qy
2272	ETSSGTSVKSTSEPESHVTKLSITSSNPSSSVPVTSPKSTPTVPESTEQPTSTTPSGQSL :	2213	Db
552	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	518	Qy
2212	GDTNSTTPSTSSLASVKSTSAPEGTSASVAPVKLSSLSPDVSQPSTKTFDATESSTVQAS	2153	DЬ
517	00G	506	Qy
2152	SVKSSPSTPSTTSQSVTSTVPETSKSTVLSSEAPVTSTSPTEVHTSSETKPSLSASSTT :	2093	Db
505	LSSSEN-	483	Qy
2092		2033	DЬ
182	4	455	Qy
2032	VSSTSATSSESTTAEPHVTTSISSTTSTKDMTSSKSPENVTMSSESPEVSTSSSKSTTAS :	1973	Db
454		455	QУ
1972	TKCENTIGSFNCVCLEGFKKVDEKCVVDEKKQPNREKIEIDEENSSSNSGQEKPTTKGI 1	1913	Db
154	EQDQRICTC	439	Qy
1912	LCAQKNDCNKHAECIDIHPDSHFCSCPDGFIGDGMICDDVDECNNAGMCDDEN 1	1860	DЪ
138	GGCDRNAECTQTGPNQAVCNCLPKYTGDGKVCSLINVCLTNNGGCSPFAFCNY 4	386	Qy
1859	EEPKSDKTACTDEWSRLCELEKKQCTVDEEEVPQCGACLPGHHP1NGTCQSLQ1SG	1800	Db
385		376	Qy
1799	GSYRCECAEGYEGEGGVCTDIDECDRGMAGCDSMAMCINRM-GSCGCKCMAGYTGDGATC	1741	Db
375		316	Qy
1740	VSCLSVRIYNGSL-SSVCECEPGFRFEKESNSCVDIDECEESRNNCDPASAVCVNTE	1685	Db
315	OGSCDCDVGWRGVKCDMEITTDNCNGTCHTSANCLLDPD	264	Qy
1684	DINECDERHPCHPHAECTNLEGSFKCECHSGFEGDGIKKCTNPLERSCEDVEKFCGRVDH 1	1625	Оb
263	TCTEGKYGIHCDQACDQAC	245	Qy
1624	CVAEKAPCSLNANCVNNNGTFSCSCKOGYRGDGFMCT	1588	Db
244	IITRACWLASLAHNAKPAPGEVKMCALGTASVWDGVNGTGTCQCGLGFNG	191	Qy
1587	KKPCDSTQSSKSHCSESNMSCEVDTVDGSVECKECMGGYKKSGKVCEDINE	1537	Db

	SN PI	TYPE: PRT	
	FILING DATE: 2002-02-21 DF SEQ ID NOS: 47374 0 5549	CURRENT F NUMBER OF SEQ ID NO LENGTH:	, .,
	F INVENTION: PLANTS WITH IMPROVED PROPERTIES FERENCE: 38-10(52052)A APPLICATION NUMBER: US/60/360,039	ITLE ILE URRE	, ., .
RODUCTION OF	<pre>: Hinkle, Gregory J. : Slater, Steven C. INVENTION: EXPRESSION OF MICROBIAL PROTEI</pre>	PPLI PPLI ITLE	
	: Chen, Xianfeng : Goldman, Barry	APPLICANT APPLICANT	
	INFORMATION: VT: Cao, Yongwei	GENERAL I	٠. ٠.
	7 .0-039-6549 .ce 6549, Application US/60360039	SULT -60-36 Sequen	(O H
	QGKLSVYCEADGMTLVLGNETADFEGKIFVK 3308	3278	Db
	QVLMSFPSLTNFLTEVLAFSKSSARGQAFLK 1211	1181	Ωу
3277	ETCADIDECAEKSHKCDRVATCRNTFGSHVCTCPDGHVGDGITCVPHVN	3229	Db
1180	0	1128	Qу
3228	FKGDFYKCSSLVSKEPANQQDLSDVSSCVTPCDSSTQLCISGECICKSGFRRNSTLSGS	3169	da
1127	K-LTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSAGWL	1074	Qy
3168	SGFSGNGVSCFPQKSCRTDKSVCAKNAICL	3129	Db
1073	ממאת	1020	0γ
3128	AHC-VGGTTCKCNPGYFGNGLCCVP-DPLDCVH-FTGICHPNAVCNSESROCQCS	3077	dd fo
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961 3076	VFAVCTPACSVHATCTENNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKV	, 912 5 3020	Db Qy
3019	FIGDGTTACSKKSTADCISLPSLCADKAKCDNSTRSCECDAGYIGDG	2973	Дb
911	FNGTACELCWHGREGPDCOPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTA	/ 857	γo
2972	TNQEEEQVTSTTTTEAPSLCSTVTCHSLATCEQSTGVCICRDG	2930	Вb
856	УТРМGQС	797	Qy
2929	SPIILPSESLTTPQPPPTTTTTAKPATTSGKRGPPSIQPPAEMFTTPAPPPPSNGGYGEE	2870	DЪ
796	CPLKS	768	Qy
2869	VTASSIPSEEPILSSVTSSSTPRVRLITGTPDDLIVSVTVPSHGNRRQNITASSVPSNST	2810	рb
767	GVAYGI	736	Qy
2809	VKLSSLFPESITSEAVTVSSRAPAEITMSSESHREISTVSSEPSEPEIPLSTTVSPNV	2752	DЪ
735	GTGSDIGELFLNEQMCRFIHRGLLF	706	Qy
2751	STENVETSTSQSGSLESSTMSSTSSEPETNAPAVTVSSEASSTTLEENSSTSSPTSSEAS	2692	Дb
705	DSKALASDLPRSASWKTLQGSELS	/ 682	Qy
2691	VSTTVSTTTPTEETTTSESLILTAAPSKPTESTTESSEAPTTPAKTSETKPSNVSSTSRK	2632	Db
681		/ 682	Qy

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                                                                    DTP--CNNRGMC-RDLYTPMGQCLCHTGF--NGTACELCWHGREGP---DCQPRSCSEH
                                                                                                                               KCIYNPLPFRRNVEGCQNLCTVVIQTPRCCHGYFMPDCQACPG-------
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20.2%;
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SEQ ID NO 5709
LENGTH: 1106
TYPE: PRT
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GENERAL INFORMATI
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Best Local
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APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10($2052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
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                                    STSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQ 531
                                                                            AEGAHCTDRDECAVE - - PCHPAAICSNTRGSYK - CECRDGFVGDGKTCHE - - -
                                                                                                                 GDGKVCSLINVCLTNNGGCSPFAFCNYTEQDQRICTCKPDYTGDGIVCRGSIYGELPKNP
                                                                                                                                                                                              TTPGNRVCVCKAGYTGD-GIVCLEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKY--T
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TILYPISNDSTVIPR--SWD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1106;
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OF.

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US-60-360-039-5866; Sequence 5866, Application US/60360039; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Caenorhabditis elegans US-60-360-039-5866
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APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5866
LENGTH: 3051
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 244; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       872 PDCQPR-SCSEHGQCDEGITGSGEC---LCETGWTAASCDTPTAVFAVCTPACSVHATCT 927
                      208 NAKPAPGEVKMCALGTASVWDGVNGTG------TCQCGLG-----FNGT 245
                                                                    869 -PRGNIYTCQCGRNEKRHPITDICLKNECLTGEHDCDRSARCIDTDESYICACQSGFIDH 927
                                                                                                                      179 GKRSVFIGCQ---
                                                                                                                                                                  818 ENERCTNDGSDWFCECLPGFERIRNGQCAYPGSCNPNDPMSCD---VRKRQQCL----- 868
                                                                                                                                                                                                133 OKNRCDNNDT------IIVRGEC---GKCSQQAPCPLETKPLRETRKCIYSIYFM 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            876 PIDRCLSRFSVPCSRNAECVESIESNPKCVCRKGYHGDGFRC 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        988 EIDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDC 1029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       797 INCESTCHCDGSVACDV-ITGM--CPGALCRAGWEGSSCD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        681 I---ENFQTKRLHIF----------TFDRVRQSGSENF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 641 HA----QFDYI-----REGLVAYT---FINDTDAVTLPL------LMRSSIGIQTAMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 652 EALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRCGTG 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             592 NLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKAL 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           706 NSFQIVLAESDKDATILSLIYEKVQARGPMTGISTPSRFLMLPNNRLASGSN-----VGQ 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGKWMYRVDIADLQTCPPG--------RLGEPLCD-----RECAAGHYG
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                                                                                                                                                                                                                                                           4.7%; Score 371; DB 7; Length 3051; ilarity 20.4%; Pred. No. 1.2e-12; Conservative 109; Mismatches 427; Indels 416;
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                                                                                                                 -PQCVRT--IITRACWLASLAH 207
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RESULT 10
US-60-360-039-5971
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RCLQDNGQCHPDASCADL 1055	MTGPGKHKCECKSHYVGDGVDCEPEQLPLDRCL	1008 1817	Qy
SC1EIDPCADGVNGGCHEHATCR 1007	KCSQKGTQVSCSCKKGYKGDGYSC	963 1757	Qy Db
NNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKVA 962	CTPACSVHATCTE	916 1697	Qy Db
CLCETGWTAASCDTPTAVFAV 915	RFGPDCQPRSCSEHGQCDEGITGSGE	869 1652	Qy Db
QCLCHTGFNGTACELCWHG 868	CNNRGMCRDLYTPMG : : NECESGVHDCDPSATCRDNEQSFT	835 1596	Qу
FEMPDCQACP834	5 -FRRNVEGCQNLCTVVIQTPRCCHGYFMPDCQACP- 	795 1540	Qy Db
CCPLKSKPKGVKKKCIYNPLP 794 :	PTLGGR-CDTFTTFDIPGECGSCIFTPKCPL	748 1482	Qy Db
CRFIHRGLLEDVGVAYGIDCLLMN 747	VRCGTG-SDIGELFLNEOM	706 1424	Qy Db
JKFHVIRDSKALASDLPRSASWKTLQGSELS 705	PTDKALEALPPEQQDFLFNQDNKDKLKSYLK : :: QLNDCHTAADCIDQVQGY	646 1405	Qy Db
YTKFSKLIQDSGLLSVITDSIHTPVTVFW 645 : :	DALGRVLQNLTTVAANHG	599 1356	Qу
ISVSQDTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPK 598 :	SATTLQGEPVSISVSQDTVFINNEAKVLSSD	543 1307	Qy Db
WDQQGLMSQVLRYHVVGCQQLLLDNLKVTT 542	AGPGPETVFAPLSSSFNHEPRIKD	489 1258	Qy Db
KPDYTG-DGIVCRGSIYGELPKNPSTSQYFFQLQEHAVREL 488	NYTEQDQRICTC TDTE-DSYICACPQSHIDL	437 1215	Оу
TGDGKVCS-LINVCLTNNGGCSPFAFC 436	GGCDRNAECTQTGPNQAVCNCLPKY 1	386 1155	Qу
TKADCKRTTPGNRVCVCKAGYTGDGIVCLEI-NPCLENH 385	AINACETSNGGCS : ::: TLNDCDSPD	335 1101	Qy Db
CACAPGERGNT 334	EITTDNCNGTCHTSANCLLDPDGKASCKCAAGFRGNGTVCT 	294 1041	Qy Db
SOGPLGDGSCDCDVGWRGVKCDM 293 :	ACETCTEGKYGIHCDQACSCVHGRCS	246 988	Qy Db
ALCTDTEEGYVCRCKSGFVDYSPNPQTFPGM 987	SPNPSERPGRVCVALQNECLDGSNRCSPNALCTDTEEGYVCRCKSGFVDYSPNPQTFPGM	928	Дb

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SEQ ID NO 5971
LENGTH: 1372
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Best Local Similarity
Matches 254; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)A CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 WLASLAHNAKPAPGEVKMCAL----GTASVWDGVNGTGTCQCGLGFNGTACE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 SPCALNATCVDLINDYKCECPTGFSGKR-----CHIKENLCASSPCVHGLCIDKLYSRQC 88
                                                                                                                           QHCQRSEEIYKGLLVRFEGFTKIIGRVERTHKSTCGVEEKSAMQKSQSQILIEDCPSDMV
                                                                                                                                                                                                            TYSNNGYATGKQLDVMTG-----ITLGSTALPSFVGSIARVGVWNRVIDFEEEL--PLMV
                                                                                                                                                                                                                                                     VTTSATTLQGEPVSISVSQDTVFINNEAKVLSSDIIST-----NGVIHVIDKLLSP---
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                                           IS-SMDRETNVTWPEPTFLSSNSKIEKIEKNLKQGQMFTWGEYDVLYTATDNATNQAQCN 696
                                                                                    ITDSIHTPVTVFWP----TDKALEALPPE---
                                                                                                                                                                                                                                                                                            LTLFPGLAAVEVPLSSSQHLNNGKWNH--LLITWQSK--
                                                                                                                                                                                                                                                                                                                                      ELAGPGPFTVFAPLSSS-----FNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLK 539
                                                                                                                                                                                                                                                                                                                                                                                                                          ----CRGSIYG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LCQPGWTGENCDQNIDECAASPCQNDAKCIDEINGY-MCECADGYEGVHCQHLVDHCAK
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                                                                                                                                                                   -KNLLITPK----DALGRVLQNLTTVAANHGYTKFSK-----LIQDSGLLSV
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·LPRSASW-KTLQGSELSVRCGTGSDI--
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                                                                                -----QQDFLFN-QDN-KDKLKSY
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PCT-US02-09671-697; Sequence 697, Application PC/TUS0209671; GENERAL INFORMATION:
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; ORGANISM: Homo PCT-US02-09671-697
                                                                                                                                                                        PRIOR EILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR FILING DATE: 2001-10-01
PRIOR PPLICATION NUMBER: 60/336,780
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
                                                                           SEQ ID NO 697
                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 08191-026W01
CURRENT APPLICATION NUMBER: PCT/US02/09671
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
                                                                                            NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-0 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: TRANSLATIONAL PROFILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                   PRIOR APPLICATION NUMBER: 60/: PRIOR FILING DATE: 2002-02-20
                                                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCAKVAKC-----SQKGTQVSCSCKKGYKGDGYSCIEIDPCADGVNGGCHEHATCRMTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPGQFLVKETKNCQFCPRGTFQNEEQESTCKLCAPDHTTAAPGATAESQCFSTNQCATGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPA-----CSVHATCTENNTCVCNL----NYEGDGIT----CTVVDFCKQNN 955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLYTPMGQCLCHTGFNGTACELCWHGRFGPDCQPRSCSEHG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDLC--VPCAPGTYHSAATGECELCPIGEYQPLTARTECFKCAPGQITASEGAISEGECK 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -NLCTVVIQTPRCCHGYFMPDCQACPGGPDTPCNNR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRRMLVDPSSGLETTIRDALHNEILSGVLNFEKVLPNGRPDVGSLKIKEEYLCQAGQVVV 929
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                                                           3494
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zycos Inc
                                                                                                                                                                                                                                                                                                                                      2001-03-28
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                                                                                                                                                         60/358,985
                                                                                              Version
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Best Local Similarity Matches 101; Conserv

Conservative

4.3%; Score 338; DB 1; 31.4%; Pred. No. 9.6e-11; ative 30; Mismatches 125

Length 3494; Indels

66;

Gaps

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Query Match

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PCT-US02-09671-703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version SEQ ID NO 703
                                                                                                                                                                                                                                                                              Matches 101;
                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: PCT/US02/09671 CURRENT FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: TRANSLATIONAL PROFILING FILE REFERENCE: 08191-026WO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/358,985
PRIOR FILING DATE: 2002-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/326,370 PRIOR FILING DATE: 2001-10-01 PRIOR APPLICATION NUMBER: 60/336,780 PRIOR APPLICATION NUMBER: 60/336,780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/279,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zycos Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3494
                                         124
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                                                                                                                                                                                                                                                                                                   Local Similarity
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ETSNGGCST--KADCKRTTPGNRVC-VCKAGYTGDGIVCLEINPCLENHGGCDRNAECTQ 396
                                                                                                                                                        FNGTACETCTEGKYGIHC-----DQACSCVHGRC----SQGPLGDGSCDCDVGW-
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                                       SSPNSPACTLD -- RDECSFQPGPCSTLVQC - FNTQGSFYCGACPTGWQGNGYICEDINEC
                                                                            ---RGVKCDMEITTDNCN---GTCHTSANCLLDPDGKASC-KCAAGFRGNGTVCTAINAC
                                                                                                                   --SYSCH-CPPETYGPQCASKYDDCEGGSVARCVHGICEDLMREQAGEPKYSCVCDAGWM 123
                                                                                                                                                                                              SFFCICPPQ------WKGPL-----CSADVNECEIYSGTPLSCQNG-GTCVNTMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGWT -- GVNCTENI - NECLSNP 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLGSLPLCTCLPGYTGNGYGPNGCVQLSNICLSHPCLNGQCID-TVSGY-----FCKCD 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGPNQAVCNCLPKYTGDG----KVCSLINVCLTN---NGGCSPFAFCNYTEQDQRICTCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EINNGGCSVAPPVECV-NTPGSSHCQACPPGYQGDGRVCTLTDICSVSNGGCHPDASCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETSNGGCST--KADCKRTTPGNRVC-VCKAGYTGDGIVCLEINPCLENHGGCDRNAECTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --SYSCH-CPPETYGPQCASKYDDCEGGSVARCVHGICEDLMREQAGEPKYSCVCDAGWM
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-03-28
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                                                                                                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                            Score 338; DB 1;
Pred. No. 9.6e-11;
0; Mismatches 125
                                                                                                                                                                                                                                                                                                                 DB 1; Length 3494;
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: NAME/KEY: misc_feature
: LOCATION: (1757)..()
: OTHER INFORMATION: Xaa =
US-10-150-821-4
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US-10-150-821-4
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APPLICANT: Elliott, Gary S.
TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 01017/37592
CURRENT APPLICATION NUMBER: US/10/150,821
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: US/09/911,842
PRIOR APPLICATION NUMBER: US/09/911,842
PRIOR APPLICATION NUMBER: US/09/911,842
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2000-08-01
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Matches 336;
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.
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ORGANISM: Mus musculus
FEATURE:
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                                                                                    GDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKDW 513
                                                                                                                                                     TQTGPNQAVCNCLPKYTGDGKVCSL-INVCLTNNGGCSPFAFCNYTEQDQRICTCKPDYT 453
                                                                                                                                                                                                               VNECQSS--PCLNNAVCKDQV-GGFSCKCPPGFLGTR--CEKNVDECLSQ--PCQNGATC
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                                                                                                                                                                                                                                                                                                    CECSLGYSGQICEENI--NECISSPCLNKGTC---TDGLASYRCTCVKGYM--GVHCETD 1333
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                                                                                                                               -KDGANSFRCQCPAGFTGTH--CELNINECQSN--PCRNQATC-VDELNSYSCKCQPGFS 1440
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Pred. No. 9.9e-11;
6; Mismatches 555
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  ---IIAANGILHIISEP--
                                                           QLVLKELASEVGVMTISCKEGHA----LQGPSVLKCLPSGQWNGSFPICKMVLCPSPPLI
                                                                                                                                                                                NGFLEHTTGRTFESEARFQCNPGYKAAGSPVFVCQANRHWHSDAPLSCTPLNCGKPPPIQ 2297
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                                                                                                GTFLRTMLGSQLLITFSQDQLHQETRFVDGRSIL----
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-LRAPPTAATAAHSGLGTGI-FCAVV-----
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RESULT 15
PCT-US02-09671-701
; Sequence 701, Application PC/TUS0209671
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LENGTH: 3623
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-698
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Best Local Similarity 31.4%;
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CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
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PRIOR APPLICATION NUMBER: 60/326,370
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR FILING DATE: 2001-12-04
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PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
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TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01
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GENERAL INFORMATION:
APPLICANT: Zycos Inc
TITLE OF INVENTION:

Inc

TITLE OF INVENTION: TRANSLATIONAL PROFILING FILE REFERENCE: 08191-026WO1

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Search completed: June 17, 2002, 12:34:07 Job time: 313 sec
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 701
LENGTH: 3623
TYPE: PRT
CORGANISM: Homo sapiens
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CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR FILING DATE: 2001-08-08
PRIOR PRIOR APPLICATION NUMBER: 60/326,370
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR FILING DATE: 2001-10-01
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR APPLICATION NUMBER: 60/338,985
PRIOR APPLICATION NUMBER: 60/338,985
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEO. 10,0002-201
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Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
<u>.</u>	524.6	11.1	664	9	BB626584	вв626584 вв626584
c 2	447.8	9.5	462	10	BF401567	BF401567 UI-R-CA0-
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4	357.6	7.6	758	10	BI838464	BI838464 603083445
ر ت	304.6	6.5	494	10	BF601840	BF601840 266924 MA
6	295.8	6.3	385	9	BB842118	BB842118 BB842118
7	287.6	6.1	462	10	BE656181	BE656181 UI-M-ВНО-
œ	253.2	5.4	459	10	T47504	T47504 yb14f01.r1
9	248.6	5.3	670	9	BB086042	BB086042 BB086042
10	245.4	5.2	1066	10	BI146461	BI146461 602913560
11	243.8	5.2	494	9	BB735524	BB735524 BB735524
12	242.2	5.1	439	9	BB847553	BB847553 BB847553
13	213.8	4.5	793	10	BI832486	BI832486 603082278
14	213.2	4.5	474	و	BB745695	BB745695 BB745695
c 15	204.4	4.3	373	10	T91781	T91781 yd52d09.s1
16	200	4.2	443	9	AA275305	AA275305 vc03d11.r
c 17	198.4	4.2	460	10	BE447169	BE447169 ut55c09.>

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BG712275 BE233224 BM148089 A2487512 BE479875	BG964207 B1006218 AA389617 AZ030878 AZ487818 AI606926 AL598662	BF660624 BG383308 B169595 AA138267 BG803514 R97483 AI272209 BBI133987	BI518863 AU080852 AU712246 BI7712246 AI852814 AA257161 BI906024 BE808086 BI183898
BG712275 pglîn.pk0 BE233224 139315 MA BE233224 T39315 MA BM148089 TCAAP1082 AZ487512 1M0317A17 BE479875 164729 BA	BG994207 602828983 B1006218 RC5-RT005 AA389617 mp25h11.r AZ030878 RPCI-23-3 AZ487818 1M0317A17 AI606926 vw30c03.x AL598662 DKFZb313N	ല വ	B1518863 603061773 AU080852 AU080852 BG712246 pg11n.pk0 A1852814 U1-M-BHO- AA257161 zr82b05.r B1966024 603062355 BB808086 Z13204 MA B1183898 UNL-P-FN-

ALIGNMENTS

	TITLE JOURNAL	VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	RESULT 1 BB626584 LOCUS DEFINITION ACCESSION
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp, Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa, K., Tawa, M., Ohara, E., watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and	, Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001) Unpublished (2001)	BB626584.1 GI:16464521 EST: house mouse. house musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 664) 1 rakawa.T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.	BB626584 BB626584 RIKEN full-length enriched, adult male diencephalon Musmusculus cDNA clone 9330210123 5', mRNA sequence.

FEATURES

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BASE COUNT
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                                                                                         ATAGACACATTGTTGTCTCCCCAAAACTTGCTTATCACCCCCAAAGGTGCCTCCGGCAGG
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="diencephalon"
/dev_stage="adult"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="9330210123"
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87.1%;
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ismatches 85;
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Qy Вb Qγ 망 δõ

source

/strain="Sprague-Dawley"
/db_xref="taxon:10116"

/organism="Rattus norvegicus"

.462

/clone="UI-R-CA0-bgm-b-05-0-UI" /clone_lib="UI-R-CA0"

/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with
polylinker; Site_1: Not I; Site_2: Eco RI;

The UI-R-CAO

modified

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF401567 462 bp mRNA U1-R-CAO-bgm-b-05-0-UI.s1 UI-R-CAO Rattus UI-R-CAO bgm-b-05-0-UI 3', mRNA sequence. BF401567 GI:11389542
                                                                                                                               The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the
                                                       normalized medulla library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-22, >AT_rich#Low_complexity
                                                                                                                                                                                                                                        451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 462)
Bonaldo, M.F., Lenno
                     Seq primer: M13 Forward POLYA=Yes.
                                                                                                                                                                                                                                                                                                  University of Iowa
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Mammalia; Eutheria;
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                                                                                                                                                                                                                             Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                    Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                       Contact: Soares, MB
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                                                                                                                                          Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 500)
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Contact: Marra M/Mouse EST Project
                                    Unpublished (1996)
                                                                         The WashU-HHMI Mouse EST Project
                                                                                                             Waterston, R.
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TAG_SEQ=GAACCG"
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TAG_LIB=UI-R-CAO
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                                                                            gaccctccaaggagagccagtttccatctctgtctctcaggacactgtgttcataaacaa 1694
                 tgaggcgaaggtcctgtccagtgacatcatcagcaccaatggcgtcatccacgttataga 1754
                                                                                                                                                                                                                                                                 tcatgagccccggattaaagactgggatcagcagggcctcatgtcccaggttcttcgcta 1574
                                                                                                                                                                                                                                                                                                                                                ccgagagettgctggacctggcccttcaccgtgttcgcgcctttgtctagctccttcaa 1514
                                                                                                                                                                                                                                                                                                                                                                                                                               ggagcttcccaagaacccttcgacgtcccagtacttcttccagttgcaggagcatgctgt 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atgtacctgcaagccagactacacgggtgatggaatcgtctgccgggggcagcatctacgg 1394
GAAGGCGAAGGTTCTGTCCAGTGACATTATCAGCACCAACGGAGTCATCCACGTCATAGA
                                                                                                                                                                                   tcacgtggtgggctgccagcagctgctgttggacaacctaaaagtgaccacaagtgccac 1634
                                                                                                                                                                                                                                              CAGTGAGTCCAAGCTTAAAGTCTGGGATAAACAGGGCCTCATGTCCCAGATTCTACGGTA
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                                                                                                                                                               {\tt TCACGTGGTGGCCTG-CAGCAGCTACTGCTGGAGAACCTAAAGGTGATCACGAGTGCCAC}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4444 Forest Park Parkway, Box 8501,
Tel: 314 286 1800
Fax: 314 286 1810
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High quality sequence stop: 465.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
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141 c
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) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; lst strand cDNA was primed with a Not I - oligo(dT)
primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
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/clone="IMAGE:1245316"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares_mammary_gland_NbMMG"
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Pred. No. 1.4
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nes 563; Conserv
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                                                                                                                                      CACATTGTTGTCTC
                                                                                  agccacagtgtgtgagaaccatcattacaagagcctgctg-tg-tggcttctttggccac
gacggtgtgaatggcactggcacgtgccagtgcgggctgggcttcaatgggacagcctgt 741
                                            http://image.llnl.gov
plate: LLAM11559 row: j column:
High quality sequence stop: 737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 758)
NIH-MGC http://mgc.nci.nih.gov/.
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BI838464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                195
                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                            Convice-"Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 0.25. Note: this is a NIH_MGC Library."

a 182 c 224 g 157 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:522506"
/clone_lib="NIH_MGC_120"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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Primates;
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Pred. No. 3.1e-68;
0; Mismatches 154;
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GATGGAGTGAATGGCACAGGTGTGTGTGAGTGTGGGGAGGGCTTCAGCGGCACAGCCTGC
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                   FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 42 row: C column: 11
Seg primer: ATTTAGGTGACACTATAG
                                                                                                                                                       Single pass sequencing. Bases v0.980904.e. Vector identified and _minmatch 12 options.
                                                                                                                                                                                                                                                                                                                    Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, U
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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Bovidae; Bovinae;
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Fax: 402 762 4390
                                                                                                                                    PCR PRimers
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Location/Qualifiers
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
                                                                                                                                                                                                       BB842118 RIKEN full-length enriched, musculus cDNA clone F430003K15 5', mEBB842118
                                                                                                        Mammalia;
                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                      Mus musculus
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                                                                                                                                                         mouse
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/db_xref="taxon:9913"
/clone_llb="MARC 3BOV"
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/lab_host="DH10B"
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336; Conserv
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-Tel: 81-45-503-9222 Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,
, Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
, RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (200
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RIKEN integrated sequence analysis (RISA) system--384-format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RIKEN full-length spleen"
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/clone="F430003K15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="6 days
97 c 110 g
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                                                 ttgagagctcctcccacggcagcaacggctgcccactctggcctggggacaggtatattc 3987
tgtgccgtcgtcctggtcactggtgcgattgctctggcagcttactcttacttccggcta 4047
                                   TTGAAAGCTCCTCCCACGGCCGCAACGGCTGCCCACTCTGGCCTAGGAACAGGCATATTC
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97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. In should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Normalization and subtraction: two approaches discovery
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UI-M-BH0-aly-h-08-0-UI.rl NIH_BMAP_M_S1 Mus
UI-M-BH0-aly-h-08-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collaborative arrangements
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301 443 1706 Fax: 301 443 9890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20892-9643, USA
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                                                                                                                    Similarity
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                                                                                                                                                                                                                               /lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI; The NIH_BMAP_M_SI library is a subtracted library derived a mixture of normalized libraries from ten regions of mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus). The driver used for subtraction consisted of a pool of 20,000 cDNA clones obtained from non-normalized and normalized libraries
                                                                                                                                                                                                                   these
                                                                                                                                                                                                                                                                                                                                                                                                  /clone="UI-M-BH0-aiy-h-08-0-UI"
/clone_lib="NIH_BMAP_M_S1"
/dev_stage="27-32 days"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   747504 459 bp mRNA linear EST 01-FEB-19 yb14f01.r1 Stratagene placenta (#93725) Homo sapiens cDNA clone IMAGE:71161 5' similar to similar to SP.A41735 A41735 HYALURONATE-BINDING PROTEIN TSG-6 PRECURSOR, mRNA sequence.
                                                                                                                                                                                                                                                                  High gality sequence stops: 308 Source: IMAGE Consortium, LLNL clone is available royalty-free through LLNL; contact the IMAG Consortium (info@image.llnl.gov) for further information. Insert Length: 1402 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other_ESTs: yb14f01.s1
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                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
Insert Size: 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                   quality sequence stop:
Location/Qualifiers
/db_xref="GDB:492058"
/db_xref="taxon:9606"
/clone="IMAGE:71161"
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                                                                                                      /organism="Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Louis,
                                                                                                                                                                                                                                                                                                                                      contact the IMAGE
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/clone_lib="Stratagene placenta

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gactgacctg-tccatccgtggcaccctgttt--gtgccacagaacagtgggctaccggg 3695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGAAGTGCTGGCCTATTCCAACAGCTCAGNTCGAGGCCGTGCATTTCTTAGGAACACNT 358
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                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 670)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Noura,K., Ohno,M., Cokazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasak,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Tagaw
                                                                       Unpublished (2001)
On Jun 21, 2000 this sequence version replaced gi:8651827
Contact: Yoshihide Hayashizaki
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Laboratory for Genome Sciences Center(GSC),
                                                                                                                                                                                      Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
Mus musculus
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                                   Exploration Research Group,
Yokohama Institute
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Computational Analysis of Full-Length Mouse cDNAs Compared with Mouse cDNAs Compared with Mouse cDNAs Compared with Computational Analysis of Full-Length Mouse cDNAs Compared with Computational Analysis of Full-Length Mouse cDNAs Compared with Mo
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 81-45-503-9216
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                                                                                                                                    Genomic Sciences Center and Genome Science Laboratory RIKEN. Division of Experimental Animal Research in Ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="diencephalon"
/dev_stage="adult"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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FEATURES

Query Match Best Local Similarity Matches 440; Conserv

Conservative

5.3%; 71.1%;

Score 248.6; Pred. No. 3.2e 0; Mismatches

2e-44; DB 9;

Length 670; Indels

35;

7;

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REFERENCE
AUTHORS
TITLE
JOURNAL
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VERSION
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BI146461
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                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
BI146461
BI146461.1 GI:
                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
                            found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM11148 row: g column: 15
                                                                                                                                                                                        Mammalia; Eutheria; Rodentia; Sc
1 (bases 1 to 1066)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa;
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quality sequence stop: 492
Location/Qualifiers
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Mus musculus
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Sciurognathi; Muridae;
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IMAGE:5054630 5',
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Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389;
                                                                                                                                                                                   musculus
BB735524
                                                                                                                                                                                                                BB735524
BB735524
l (bases 1 to 494)
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.
                                                                                                                                                   EST
                                                                                   Mammalia;
                                                                                               Eukaryota; Metazoa;
                                                                                                                   Mus musculus
                                                                                                                                   house mouse
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/db_xref="taxon:10090"
/clone="ib="MAGE:5054630"
/clone=lib="MAGE:5054630"
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Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."

72 a 330 c 276 g 188 t
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/organism="Mus musculus"
                                                                                  Eutheria;
                                                                                                                                                                  GI:16134674
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                                                                                  Chordata;
Rođentia;
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Pred. No. 1.7e
0; Mismatches
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No. 1.7e-43;
                                                                                  Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                                                     Murinae;
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 TGGTTAGTCTGGGGTTGTCGTCATGGGTAAGGGGACATGTTTCCAGGACACC - AGTATAC
                   tggttaatctgggattgtcgccagggctaaggagccatgttgcctggatacctgggggac
                                                                                                 encyclopedia: real-time sequence clustering for construction on nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues.
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
Contact: Yoshihide Hayashizaki
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RIKEN integrated sequence analysis (RISA) system--384-format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="spleen"
/dev_stage="6 days neonate"
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/clone="f430003K15"
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/strain≂"C57BL/6J"
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Pred. No. 3.5e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carnincip./ Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carnincip., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tanaka,T., Matsuura
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
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Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.
encyclopedia: real-time sequence clustering for construction o
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                           Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                              Shibata, K., Itoh, M.,
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                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 793)
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                                                                                                                                                             mRNA sequence.
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http://mgc.nci.nih.gov/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Site_1: XhoI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="F530009M16"
/clone_lib="RIKEN full-length enriched, adult male kidney"
/sex="male"
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/dev_stage="adult"
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/db_xref="taxon:10090"
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83.3%;
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Pred. No. 7.9e
0; Mismatches
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                                       Hominidae;
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POCOS.

SOURCE

Eukaryota;

Metazoa;

Chordata; Craniata;

Vertebrata;

Euteleostomi;

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                                                                                       DEFINITION
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JOURNAL
 ORGANISM
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                             gtagactacggatccagggccaacaagagtgaaatgtgggatgtcttctgttaccggatg 3471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGGTTGCCTACCCCACAGCCTTCGCCTCCCAGAACTGTGGCTCTGGTGTGGGTTGGGATA 312
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                                                                         BB745695 arken full-length enriched, ad cDNA clone F530009M16 3', mRNA sequence
Mus musculus
                                           BB745695
BB745695.1 GI:16148634
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    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc
                              EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://image.llnl.gov
Plate: LLAM11556 row: 1 column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Institutes of Health,
                house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source anonymous pool of spleen and pancreas from 28 yo male. Library is ollgo-dT primed and directionally clons (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 0.25. Note: this is a NIH_MGC Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:5221410"
/clone_lib="NIH_MGC_120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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84.1%;
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Pred. No. 1.5e-
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BASE COUNT
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  Best Local Sin Matches 364;
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Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii
, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Tagawa
, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
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Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y. and Hayashizaki,Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Konno, H., Fukunishi, Y.,
                                                                                                                                                       101
     Conservative
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/dev_stage="adult"
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/clone="F530009M16"
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                          4.5%;
76.5%;
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135 c 119 g 119 t
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     0;
Score 213.2; DB 9;
Pred. No. 1.9e-36;
0; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                  DB 9;
                                               Length 474;
     Indels
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High quality sequence stops: 283 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llni.gov) for further information. Insert Length: 710
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The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
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Notch homolog prot
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fibropellin Ia - s
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
335	338	343	344	344	348	348	348.5	348.5	355.5	357.5	359.5	371	373.5	375.5	392
4.3	4.3	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.5	4.5	4.6	4.7	4.8	4.8	5.0
3672	3623	3075	3084	1786	4544	1801	2139	1786	3106	1133	1372	3051	1106	1584	1220
2	N	2	-	_	ш	ب	2	Н	_	ب	2	2	N	Ν	N
T23433	T09456	S14458	MMMSA	MMHUB1	S02392	MMRTS	A35672	MMMSB1	S53868	EGRT	T25933	S42373	T18739	T22674	A56136
hypothetical prote	intrinsic factor-E	laminin alpha-1	laminin alpha-1	laminin beta-1 cha	alpha-2-macroglobu	laminin beta-2 cha	crumbs protein -	laminin beta-1 cha	laminin alpha-2 c)	epidermal growth	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	jagged protein pre

ALIGNMENTS

hypothetical protein DKFZp434E0321.1 - (Species: Homo sapiens (man) C:Date: 11-Jan-2000 #sequence_revision C:Accession: T42681 R:Blum, H.; Bauersachs, S.; Mewes, H.W.

11-Jan-2000 #text_change 11-Jan-2000

Wiemann,

human (fragments)

H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.;

RESULT

DЬ Qy Qy Db δÃ Qy A:Status: preliminary
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Moslecule type: mRNA
A:Residues: 1-870:871-1069 <AAA>
A:Cross:references: EMBL:ALl33021
A:Experimental source: adult testis; clone DKFZp434E0321
A:Note: the cDNA sequence contains a +1 frameshift near codon
C:Genetics:
A:Note: DKFZp434E0321.1 submitted to the Protein Sequence Database, November A; Reference number: Z22233
A; Accession: T42681 Ş В Вþ 밁 δÃ Ъ 9 Query Match Best Local Similarity Matches 798; Conserv 676 616 556 496 316 GKASCKCAAGERGNGTVCTAINACETSNGGCSTKADCKRITPGNRVCVCKAGYTGDGIVC 366 306 246 186 376 66 6 GTASCKCAAGFQGNGTICTAINACEISNGGCSAKADCKRTTPGRRVCTCKAGYTGDGIVC 65 KEHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDV 735 LEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKYTGDGKVCSLINVCLTNNGGCSPFAF 435 GYIKESNLIQDSGLLSVITDP1HTPVTLFWPTDQALHALPAEQQDFLFNQDNKDKLKEYL GYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYL 675 VFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSIS VFAPLSAAFDEEARVKDWDKYGLMPQVLRYHVVACHQLLLENLKLISNATSLQGEPIVIS 56.6%; Score 4447.5; DB 2; Length 1069; ilarity 73.1%; Pred. No. 2.7e-268; Conservative 100; Mismatches 146; Indels 47; Gaps 245 365

736

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RESULT 2
A55624
R;Yin, W.; Smiley, E.; Germiller, J.; Sanguineti, C.; Lawton, T.; Pereira, I
J. Biol. Chem. 270, 1799-1806, 1995
A;Title: Primary structure and developmental expression of Fbn-1, the mouse A; Accession: A55624; MUID:95130561
A;Accession: A55624; MUID:95130561
                                                                            A;Molecule type: mRNA
A;Residues: 1-2871 <YIN>
A;Cross-references: GB:L29454; NID:g575509;
C;Genetics:
A;Gene: Fbn-1
C;Superfamily: unassigned EGF-related protei
E;1201-1236/Domain: EGF homology <EGF>
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                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTGAVALAAYSYFRINRRTIGFQHFESEEDINVAALGKQQPENISNPLYESTTSAPPE--
              Similarity
   Conservative
                                                                            ed EGF-related proteins;
homology <EGF>
            6.5%;
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 130;
Score 510; DB 2;
Pred. No. 3.7e-23;
0; Mismatches 416
                                                                                                                                         PIDN: AAA56840.1;
                                                                                            EGF
 416;
                                                                                            homology
                             Length 2871;
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Indels
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612;
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                NECELSANLCPHGRCVNLIGKYQCACNPGYHPTHDRLFCVDIDECSIMNGGCETFCTNSD 1216
                                                                                                                                       --DIDECRISPDLCGR
                                                                                                                                                                                                     KDINECKMIPSLCTHGKCRNTI--GSFKCRCDSGFALDS---EERNCT
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                                                                                                         NPLPFRRNVEGCQNLCTVVIQTPRCCHGYFMPD-----
                                                                                                                                                                     AYGIDCLLMNPTLGGRCDTFTTFDIPGECGSCIFTP-----KCPLKSKPKG--VKKKCIY
                                                                                                                                                                                                                                    HVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGV
                                                                                                                                                                                                                                                                  IAGRHRMDACCCSVGAAWGTEECEECPLRNSREYEELCPRGPGFA----TKDITNGKPFF
                                                                                                                                                                                                                                                                                                                                                             ISTNGVI---HVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLS 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLD-NLKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGVCKNSPGSF - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGGC--SPFAFCNYTEQDQRICTCKPDYTGD--GIVCRGSIYGELPKNPSTSQYFFQLQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQNSAEYQALCSSGPGMTSAGTDINECALDPDICPNGICENLRGTYKCICNSGYEVDITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----INEDGSFKCICKPGFQLASDGRYCKDINECETPGICMNGRCVNTDGSYRCECF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTSANCLLDPDGKASCKCAAGFR--GNGTVCTAINACET----SNGGC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDECLQNGRICNNGRCIN---TDGSFHCVCNAGFHVSSEGKNCEDMDECRTPNMCPNGMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIHCDQ-ACSCVHGRCSQGPLGDGS--CDCDVGW----RGVKC-DM-EITTDN-C-NGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RCECNKGFQLDIRGECIDVDECEKNPCTGGECINNQGSYTCHCRAGYQSTL--TRTECRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QPVPPGYPPGPVIPVPRPPPEYLYPSREPPRVLPVNVTDYCQLVRYLCQNGRCIPTPGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITKMQCCCDLGRCWSPGVTVAPEMCPIRSTEDFNKLCSVPLVIPGRPEYPPPPIGPLPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATDKGVIHGLEKVLEIQKNRC------DNNDTIIVR-GEC-----GKCSQQAP--
                                              ---YTPMG---
                                                                            -DIDECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -CPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ICECSPESTLDPTKTICIETIKGT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -KRTTPGNRV-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -EVKMCALGTASVWDGVNGTG--TCQCGLGFNGTACETCTEGKY
                                                                                                                                                                                                                                                                                                                                                                                                                           -GEPVSI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSVFIGCQPQCVRTI-ITRACWLAS-LAHNAK--PAPG---
                                                                            RDPLLCRGGICHNTEGTYRCECPPGHQLSP--NISACIDI
                                             -QCLCHTGFNGT - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ETKPLRET----RKCIYSIYFMGK------
                                                                                                                                         -GQCVNTPGDFECKCD-EGYESGFMMKNCM-
                                                                                                                                                                                                                                                                                                -KALEALPPEQQDFLFNQDNKDKLKSYLKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -STKADC--
                                                                                                         -CQACPGGPDTPCNNRGMCRDL
                                                                                                                                                                                                                                                                                                                                                                                                                       -SVSQDTVFINNEAKVLSSDI
                                                                                                                                                                                                                                                                                                                                --- ETCFLKYDDEECTLP
                                             ------ACE-LCWH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CWQTVIDGRCEIN
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1026

677 970 574

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865

482

817 426 760 372

852

700

352 640 346 587 304 530 255 472

214

180 352

of extrace

2000 L.Y.	RESULT 4 A47221 A47221 fibrillin 1 precursor - human (fragment) C;Species: Homo sapiens (man) C;Ste: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 21-Jul- C;Accession: A47221; 154355; S17064; 159574; S17062; S62111; A34198 R;Corson, G.M.: Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, Genomics 17, 476-484, 1993	
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76	1119 VAYPTTYASOKOGANVUGIVNYGSRANKSEMWNVECYBMKNVNCTCKAGYVGDG-ESCS 1	_
1551	QY 1000 "GVEHLEGETGGICTETECHAREACA"" NEARLETINGLISTAGNAKTHUCSAGWLESGK Db 1503 POWEHCTODDG-VELDRIGGNATDTDECADDTNAVAGTAVATGRAVEG-CNC Db 1503 POWEHCTODDG-VELDRIGGNATDTDECADDTNAVAGTAVATGRAVEG-CNC	
, ,	1062 - OUD III DANG TOLONG VILLENGE VIL	
1502	OY 1036 LDRCLODNOCC	
4 1	1303 KEGWYGNGINCIDLDCANGIH-QCSINAQCYNI-FGSIKCACSEGFIGDGFICSD	
03	976 KKGYKGDGYSCIEIDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDCEPEQLP :: : :	
1388	HCQLGYSVKKGTTGCTDVDECEIGAHNCDMHASCLNVPGSFKCSC	
975	HATCTENNTCVCNLNYE-GDGIT-CTVVDFCKQNNGGCAKVAKCSQKGTQVSCSC	
1329	DIC-DGGQC-TNIPGEYRCLCYDGF-MASMDMKTCIDVNECDLNPNIC	
921	HGQCDEGITGSGECLCETGWTAASCDTPTAV-FAVCTPACS	
1279	GCDTQCTNSEGSYECSCSEGYALMPDGRSCADIDE	
864	DCQACPGGPDTPCNNRGMCRDLYTPMGQCLCHTGFNGTACEL	
1226	LGHELSPSREDCVDINECSLSDNLCRNGKCVNMIGTYQCSCNPGYQA	
820	PKGVKKKCI-YNPLPFRRNVEGCQN-LCTVVIQTPRC-CH-GY-F	
1175	KNCMDIDECERNPLLCRGGTCVNTEGSFQ	
765	VAYGIDCLLMNPTLGGRC-DTFTTFDIPGE	
1119	IDECRISPDLC	
727	QGSELSVRCGTGSDIGELFLNEQMCRFI	
1064	C	
677	IHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKF-	
1008	Db 962 GRCVNSKGSFHCECPEGLTLDGTGRVCLDIRMEHCFLKWDEDECIHP	
631	STNGVIHVIDKLLSPKNLL1TPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLS	
961	DAACPRGFARIKGVTCEDVNECEVFPGVCPN	
571	QLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAKVLS	_
924	Db 892 WLNIQDNRCEVNINGATKSECCATLGGA	
516	PKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQ	_
891	Db 839 ETETCEDVNECESNPCVNGACRNNLGSFHCECSPGSKLSSTGLICIDSLKGTC	
465	OGKVCSLINVCLTNNGGCSPFAFCNYTEQDQRICTCKPDYTGDGIVCRGSIYG	
838	YEPDASGRNCIDIDECLVNRLLCD-NGLCRNT-PGSYSCTCPPGYVLPT	
412	YTGDGIVCLEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKYTG	_

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A; Map PUBLION. 1978-1. 2797/1
A; Introns: 2286/1; 2297/1
A; Introns: 2286/1; 2297/1
C; Superfamily: unassigned EGF-related proteins; EGF homology
C; Superfamily: unassigned EGF-related proteins; EGF homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 1166-1176, 'X',1178-1180, 'D',1182-1185 <LEE2>
R; Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.
J. Biol. Chem. 264, 21381-21385, 1989
A; Title: Connective tissue microfibrils. Isolation and characterization of three lar A; Reference number: A34198; MUID:99078246
A; Reference number: A34198
A; Accession: A34198
A; Molecule type: protein
A; Residues: 565-575;1890-1892, 'I',1894-1900 <MAD>
C; Comment: Fibrillin is a major component of elastin-associated microfibrils.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL;X63556
R;Dietz, H.C.; Valle, D.; Francomano, C.A.; Kendzior, R.J.
Science 259, 680-683, 1993
A;Title: The skipping of constitutive exons in vivo induced by nonsense mutations.
A;Reference number: I59574; MUID:93157831
A;Accession: I59574
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A;Residues: 1-337, Tr', 339-1029 <COR>
A;Cross-references: GB:X63556
R;Perelra, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.;
Hum. Mol. Genet. 2, 961-968, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:S54426; NID:g264860; PIDN:AAB25244.1; PID:g264861 R;Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M. Nature 352, 330-334, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 2217-2288,'I',2290-2325 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:L13923; NID:g306745; PIDN:AAB02036.1; R;Maslen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Nature 352, 334-337, 1991
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A;Residues: 132-3002 <PER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hum. Mol. Genet. 2, 961-968, 1993
A;Title: Genomic organization of the sequence coding for fibrillin, the defective ge
A;Reference number: 154355; MUID:93372860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain str A;Reference number: A47221; MUID:94010947 A;Accession: A47221
                                                                                                   QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 'VLVTVVFIFLSYNKML', 944-1444 <LEE1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Linkage of Marfan syndrome and a phenotypically related disorder to two difa;Reference number: $17062; MUID:91304567
A;Accession: $17062
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A; Residues: 1030-3002 <MAS>
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A;Accession: S17064
                                       Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                              Matches
                                       573
                                                                                                       189 PQCVRTIITRACWLAS-LAHNAK--PAPG------EVKMCALGTASV 226
                                                                                                                                                                                                               Local Similarity
                                       PRVLPVNVTDYCQLVRYLCQNGRCIPTPGSYRCECNKGFQLDLRGECIDVDECEKNPCAG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15q21.1-15q21
                                                                                                                                                                              Conservative 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDB:127115; OMIM:134797; OMIM:154700
                                                                                                                                                                                                               6.3%;
21.7%;
                                                                                                                                                                Score 497.5; DB 2;
Pred. No. 2.3e-22;
""smatches 356;
                                                                                                                                                                                                                                           Length 3002;
                                                                                                                                                                           Indels 465;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sarfarazi, M.; Tsipouras
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Sakai, L.Y.
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uctu	Qy	227 WDGVNGTGTCQCGLGFNGTACETCTEGKYGIHCDQ-ACSCVHGRCSQGPLGDGSCD 281	31
	Db	633 GECINNOGSYTCOCRAGYOSTL TRTECRDIDECLONGRICHNGRCINTDGSEHCV 687	37
	Оу	CDVGWRGVKCDMEITTDNCNGTCHTSANCLLDPDGKASCKCAAGFRG	328
onac	Db	688 CNAGEHVIRDGKNCEDMDECSIRNMCLNGMCINEDGSFKCICKPGFQLAS /3/	3/
ne p	Qy	329 NGTVCTAINACETSNGGC3	346
	Db	738 DGRYCKDINECETPGICMNGRCVNTDGSYRCECFPGLAVGLDGRVCVDTHMRSTCYGGYK 7	797
	Qy	347KRTTPGNRV 3	361
	рь	798 RGQCIKPLFGAVTKSECCCASTEYAFGEPCQPCPAQNSAEYQALCSSGPGMTSAGSDINE 8	857
	Qy		398
	дb	858 CALDPDICPNGICENLRGTYKCICNSGYEVDSTGKNCVDINECVLNSLLCD-NGQCRNT- 915	5
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	рb	916 PGSFVCTC-PKGFIYKPDLKTCEDIDECESSPCINGVCKNSPGSFICECSS 965	Š
	Qy	451 DYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEP 508	80
	ф	966 ESTLDPTKTICIETIKGT9	983
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	Db	984CWQTVIDGRCEININGATLKSQCCSSLGAAWGSPCTL-C 1	1021
, TO	Qy	557 SQDTVFINNEAKVLSSDI	96
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	Dр	1129 MRNTPEYEELCPRGPGFATKEITNGKPFFKDINECKMIPSLCTHGKCRNTIGSF 1	1182
n n	Qy	705 SVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGVAYG 7.	740
, (Db		1239
	Qy		782
	Db	INTEGSYRCECPPGHQLSPNISACIDINECELSAHLCPN	1299
	Qy		820
	Db	1300 GRCVNLIGKYQCACNPGYHSTPDRLFCVDIDECSIMNGGCETFCTNSEGSYECSCQPGFA 1:	1359
	Qy	821 -MPDCQACPGGPDTPCNNRGMCRDLYTPMGQCLCHTGFNGTACELCWHGRFG 8	871
ted	Db		1404
	Оy	872 PDCQPRSCSEHGQCD	917
	рb	1405 DMKTCVDVNECDLNPNICLSGTCENTKGSFICHCDMGYSGKKGKTGCTDINECEIGA 1	1461
<u> </u>	Qy		972
	Db	1462 HNCGKHAVCTNTAGSFKCSCSPGWIGDGIKCTDLDECSNGTHMCSQHADCKNTMGSYR 1	1519
	Qy	HATCRMTGPGKHKCECKSHYVGDG	1026
	Db	1520 CLCKEGYTGDGFTCTDLDECSENLNLCGNGQCLNAPGGYRCECDMGFVPSADG 1	1572
_	Qy	1027 VDCEPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAK 1	1082

635	578 NGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITD	Qy
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577	518 LMSQVLRYHVVGCQQLLLLDNLKYTTSATTLQGEPVSISVSQDTVFINNEAKVLSSDIIST	Qy
516	505 C	Db
517	459 CRGSIYGELPKNPSTSQYFFQLQEHAVRE-LAGPGPFTVFAPLSSSFNHEPRIKDWDQQG	Qy
504	403 VCNCLE*-KYTGDGAVCSLINVCLTNNGGCSPFAFCNYTEQDQRICTCKPDYTGDGTV	Db 43
447	94 TCHKLCMHLDSGHVQCFCDDGYELIDSKFCQDINECHENNGDCSQIC	Db
402	369TGTGDGIVCLEINPCLENHGGCDRNAECTQTGPNQA	Qy
393	335 -QHDCYDQPDCGHVCKCRNGYILANDQKLCHDNISTVIHARAPRLWDSYETVTCVTPTDL	Db
368	348 TKADCKRTTPGNRVCVCKAGY	Qу
347	295 -ITTDNCNGTCHTSANCLLDPDGKASCKCAAGFRGNGTVC-TAINACETSNGGCS :	Qу
279		Db !
	243NGTACETCTEGKYGIHCDOACSCVHGRCSOGPLGDGSCDCDVGWRGVKCDWE-	Oy
242	229 G-VNGTGTCQCGLGF	Оy
170	125 GGCEHECVNTIGTYYCRCWPGFELSGDGNTCSDIDECAVSNGGCSD	Dβ
228	182 SVF1GCQPQCVRTIITRACWLASLAHNAKPAPGEVKMCALGTASVWD	Qy
181 124	129 VLEIQKNRCDNNDTIIVRGECGKCSQQAPCPLETKPLRETRKCIYSIYFMGKR	Qy Db
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1; 601/1; 625/1; 7	Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1	A; Int
	spetics: one- (ESS)-V64C10A f	C;Gene
:Y64G10A.f	ossiques: 171040 kMLD: Cossineferences: EMBL:ALL10498; NID:e1542303; PIDN:CAB54471.1; CESP: Therimantal source: clone v6/67104	A; Cro
	olecule type: DNA sidnes: 1-1600 /urr	A; Mol
		A; Acc
	nitted to the EMBL Data Library, September 1999	submi
-1999	hypothetical protein Y64G10A.f - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct C;Accession: T27283	hypot C;Spe C;Dat
	JLT 5 283	RESUL'
	1614 GNC 1616	Db
	1083 EAC 1085	Qy
1613	1573 KACEDIDECSLPNICVFGTCHNLPGLFRCECEIG-YELDRSG	Db

4. 4.	A; 7 A; 7 A; 8	J. R; 2	000	A54 fik	D 17 C	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Оу	Db	Qy	Db	Qy	Db	Оy	DЪ	Qy	Db	Qy	Db	Qy	Db
Status: p	A:Title: Structure and expression of fibrillin-2, a novel microfibrillar component pr A:Reference number: A54105; MUID:94165150 A:Accession: A54105	J. Cell Biol. 124. 855-863. 1994	C:Species: Homosapiens (man) C:Species: Homosapiens (man) C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 17-Nov-2000	A54105 fibrillin-2 precursor - human	DEC. II.	1287 DPISGH	1171	Db 1254 PGWSGEHCEKSCVSGHYGAKCEETCECENGALC 1286	1111 AGWLESGRVAYPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGY	Db 1211 ECIDCWTGPSLCPFGQFGRNCAQRCNCKNGASCDRKTGRCECL 1253	1051 SCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACA	Db 1151 SCQCSNGASCDRVTGFCDCPSGFMGKNCESECPEGLWGSNCMKHCLCMHGGECNKENGDC 1210	1016CECKSHYVGDGVDC	Db 1091 FGEGCNAICDCTTTNDTSMYNPFVARCDHVTGECRCPAGWTGPDCQTSCPLGRHGEGCRH 1150	997 NG-GCHEHATCRMTGP	Db 1039 CDETCDSGLFGAGCKGICSCQNGATCDSVTGSCECRPGWRGKKCDRPCPDGR 1090	943 ITCTVVDFCKQ	985 CECAPGWSGKKCDKACAPGTFGKDC	895 CLCETGWTAASCDTPTAVFAVCTPAC	Db 928 SCYNGAKCDESDGSCHCTPGFYGATCSEVCPTGRFGIDCMQLCKCQNGAICDTSNGS 984	849 -	Db 868 HKSKVCHHVTGTCTCLPGKTGPLCDQCLIFVETIEFDIAFSINVIACAPNTYGPNCAHTC 927	Qy 848 M 848	Db 808 AGCAMKCSCPAGIRCDPVTGDCTKKCPAGYQGNLCDQPCPAGYFGYDCEQKCSCADVASP 867	826PDTP	Db 755 PCPHFTFGKNCRFPCKCARENSEGCDEITGKCRCKPGYYGHHCKRMCSPGLFG 807	792 PLPFRRNVEGCQNLCTVVIQTP	Db 701 CEDPEKCSDGPCPDGFYGSQCNLKCRMDCPNGRCDPVFGYCTCPDGLYGQSCEK 754	754 CDTFTTFDI	647 KCSMRGSGLLSKCDCP	696 WKTLQGSELSVRCGTGSD-IGELFLNEOMCRFIHRGLLFDVGVAYGIDCLLMN	Db 617 EVRTDPSEKCPNGFFGSTCQLSCSDCQNGG 646	636 SIHTPVTVFWPT	Db 564 SKVPGLDSIDEVIS SIESYPADESPRPLVFGRRRHVKACVNFQGTLSLELFSS 616

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F;1-29/Domain: signal sequence #status predicted
F;30-2918/Product: fibrillin-2 #status predicted
F;1245-1280/Domain: EGF homology <EGFI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 752-1407,'R',1409-1489,1791,'GS',1794-1796,'QLI',1922-1923,'LD',1926,'P',19
A;Cross-references: EMBL:X62009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: S31101
A; Accession: S31101
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A; Residues: 752-1489,1791,'GS',1794-1796,'QLI',1922-1923,'LD',1926,'P',1928
A;Cross-references: EMBL:X62009
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A; Cross-references: GB: U03272
A; Cross-references: GB: Vitale,
R:Lee, B.; Godfrey, M.; Vitale,
Nature 352, 330-334, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Milewicz, D.M.
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                                   VIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSV----ITDSIH
                                                                         --CERCELDT-ACPRGLARIKG----
                                                                                                             VGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAKVL - - - - - SSDIISTNGVIH
                                                                                                                                                     WLNIQDSRCEVNINGATLKS-----ECCATLGAA-------WGSP-----
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----CECPEGLTL---DGTGRVCLD---IRMEQCYLKWD---EDECIHPVPGKFRMDACC
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Pred. No. 2.6e-22;
27; Mismatches 400;
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1026 CAVGAAWGTECEBCCPKPGTKEYETLCPRGAGF ANRGDVLTGRPFYKDINECKAFPGM 690 LPRSASWKTLQGSELSVRCGTG	Db	D D D D D D D D D D D D D D D D D D D	Qy Db	Db Qy Qy Ob	
CAVGAAWGTECEECCRRGTKEYETLCPRGAGFANGDULTGRRPFYKDINECKAFPG LPRSASWKTLGSELSVRCGTGSDIGELFLNEOMCREIHRGLLFDVGAFPG CTYGKCRNTIGSFKCRCNSGFALDMEERNCTDIDECRISPDLCGSGICVNTPGS GIDCLLMNPTLGGRC-DTFTTFDIPGECGSCIFTPKCF	1452 1065 1512	1341 979 1398 1039		740 1138 778 7187 1187 829	1026 690 1083
M 1082 Y 739 E 1137 L 777 L 1777 L 186 - 828 D 1244 D 179 D	CAENINLCENGOCLNVPGAYRCECEMGFTPASDSRSCQDIDECSFQNICVSGTCNNLPGM FHLRSPLGOYKLTFDKAKEACAKEAATTATYNOLSYAQKAKYHLCSAGWLESGRVAY	ENTKGSFICHCQLGYSVKKGTTGCTDVDECEIGAHNCDMHASCLNIFGSFKCSCREG YKGDGYSCIEIDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDCEPEQLPLDR		GIDCLLMNPTLGGRC-DTFTTFDIPGECGSCIFTPKCPL 777	639 TPYTYEWPTD

Cell 66, 649-661, 1991
A;Title: TAN-1, the human homolog of the Drosophila A;Reference number: A40043; MUID:91347367
A;Accession: A40043 notch protein homolog TAN-1 precursor - human C;Species: Homo sapiens (man) C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 13-Aug-1999 C;Accession: A40043 A;Cross-references: GB:M73980 C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol F;261-292/Domain: EGF homology <EGX1> F;494-525/Domain: EGF homology <EGF1> F;1960-1992/Domain: F;1994-2026/Domain: F;1149-1180/Domain: F;1187-1218/Domain: F;987-1018/Domain: EGF homology <EGX2> A; Molecule type: mRNA A; Residues: 1-2555 <ELL> R; Ellisen, L.W.; Bird, J.; West, F;1927-1959/Domain: F;1233-1264/Domain: A; Status: preliminary; nucleic acid sequence 2060-2092/Domain: 2027-2059/Domain: i: EGF homology <EGF> : EGF homology <EGF3> : EGF homology <EGX3> : ankyrin repeat homology < i: ankyrin repeat homology < ankyrin ankyrin repeat repeat D.C.; homology homology Soreng, A.L.; <AN2>
<AN3>
<AN4> <AN5> <AN1> not shown; not Notch gene, Reynolds, compared with T.C.; Smith, S.D.; is broken by conceptual

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3	LNYEGDGITC-TVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIEI 989	y 936 b 1049	Ф
88	SEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVC-TPACSVHATCTENNTCVCN 935	у 880 b 993	Db Qy
	CHTGENGTACEPDCQPRSC 879	y 853 b 933	Qy Db
.5 10	NLCTVVIQTPRCCHGYFMPDCQACPGGPDTPCNNRGMCRD-LYTPMGQCL 852	у 804 b 886	da Vo
J. W	IPGECGSCIFTPKCPLKSKPKGVKKKCIYNPLPFRRNVEGCQ 803	y 762 b 833	Оy
	GTGSDIGELFLNEQMCRFIHRGLLFDVGVAYGIDCLLMNPTLGGRCDTFTTFD 761	y 709 b 779	Оy
w	QDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRC 708	y 659 b 726	dd Vo
5. W	DALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITDS1HTPVTVFWPTDKALEALPPEQ 658	y 599 b 694	da Vo
<u> </u>	KVTTSATTLQGEPVSISVSQDTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPK 598	y 539 b 652	Оy
, w	AVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNL 538	y 484 b 623	DP DP
	GGCSPFAFCNYTEQDQRICTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEH 483	y 428 b 567	Оу Д
ÿ. 7	YTGDGIVCLEINPCLENHGGCDRNAECTOTGPNQAVCNCLPKYTGDGKVCSLINVCLTNN 427	у 368 b 520	Qу Дъ
	PDGKASCKCAAGFRGNGTVCTAINACETSNGGCSTKADCKRTTPGNRVCVCKAG 367	y 314 b 470	Db Db
	YGIHCDQACSCVHGRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNC-NGTCHTSANCLLD 313	y 255 b 420	ОУ
-	-PAPGEVKMCALGTASV : : CPHGRTGLLCHLNDACI	y 211 b 361	9d Vo
0 0	KCIYSIYFMGKRSVFIGCQPQCVRTIITRACWLASLAHNAK 210	y 170 b 310	DP 6A
	EKVLEIQKNRCDNNDTIIVRGECGKCSQQAPCPLETKPLRETR 169	y 127 b 256	ОУ
74;	Match 6.3%; Score 492; DB 2; Length 2555; ocal Similarity 21.7%; Pred. No. 4.2e-22; s 269; Conservative 120; Mismatches 445; Indels 406; Gaps	Query Mata Best Loca Matches	

N;Alternate names: neurogenic repetitive locus C;Species: Drosophila melanogaster

protein

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A24420; A24768; S09358; A05267

MUID:87064624

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                                                                                                                                                                                                                                                                                                          GTCQDSYGTYKCTCPQGY--TGLNCQNLVRWC--DSSPCKNGGKCWQTNNFYRCECKSGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTCKDQI-----NGFTCVCPDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGVNCETKIDDCASNLCDNGKCIDKIDGYECTCEPGYTGKLC---NININECDSNPCRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPCHYGTCKDGIATFTCLCRPGYTGRLCDNDINECLSKPCLNGGQCTDRENGYICTCPKG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RCDCPTGFSGNLCQHDFDECTSTPCKNGAKCLDGPNSYTCQCTEGFTGRHCEQDINECIP 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---STSQYFFQLQEHAVRE-----LAGPGPFTVFAPLSSSFNH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N--PCQNDSTC-LDQIGEFQCICMPGY--EGLYCETNI-DECASNPCLHNGKCIDKINEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNGGCSPFAFCNYTEQDQRICTCKPDYTGDGIVCRGSIYGELPKNP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DMTGAYICT-CKAGFSGPNCQTNINECSSNP--C--LNHGTCIDDVAGYKCNCMLPYTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVITD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVFINNEAKV--LSSDIISTNGVIHVID------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DWDQQGLMSQVLRYHVVGCQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGP--ACNNDVDECSLGANPCERGGRCTNTLGSFQ--CNCPQGYAGPR--CEIDVNECLS
                                                                                                                ATYNQLSYAQKAK---YHLCSAG-----WLESGRVAYPTTYASQKCGANVVGIVDYGSRA
                                                                                                                                                    --- VDEC -- SPNPCQNGATCTDY ---
                                                                                                                                                                                       QLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATI
                                                                                                                                                                                                                             TGYYCDYPSVSC-EVAAKQQGVDIVHLCRNSGMCVDTG-NTHFCRCQAGYTGS--YCEEQ
                                                                                                                                                                                                                                                     KG-----DGYSCIEIDPCADGVN--GGCHEHATCRMTGPGKHKCECKSHYVGDGVDCEPE
                                                                                                                                                                                                                                                                                                                                             ATCTEN----NTCVCNLNYEGDGITC-TVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGY
                                                                                                                                                                                                                                                                                                                                                                                                                       LCWHGRFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NMFFCN-CPAGFRGPKCEEDINECASNPCKNGANCTDCVNSYT----CTCQPGFSGIHCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FMPDCQACPGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QNTNGSYKC -- NCKPGYTGRNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ICEAVLAPCAGSPCKNGGRCKESEDFETFSCECPPGWQGQTCEIDMNECVNRPCRNGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----MNPTL-----GGRC---DTFTTFDI---PG-----ECGSCIFTP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLQGSELSVRCGTG--
                               NKSEMWDVF-----CY----
                                                                                                                                                                                                                                                                                                                                                                                   ----SNTPDCTESSCFNGGTCIDGI-NTFTCQCPPGFTGSYCQHD--INECDSKPCLNG
                                                                           AGYHGVNCSEEINECLSHPCQNGGTCIDLINTYKCSCPRGTQGVHCEINVDDCTPF----
YDSFTLEPKCFNNGKCIDRVGGYNCICPPGFVGE--RCEGDVNECL 1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KCPLKSKPKGVKKKCIYNPLPFRRNVEGCQNLCTVVIQTPRCCH-----GY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SDIGELFLNEQMCRFIHRGLLFDVGVAYGIDCLL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----PDTPCNNRGMCRDL---YTPMGQCLCHTGFNGTACE
                                   -RMKDVNCTCKAGYVGDGFSCSGNLLQVL 1183
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                                                                                                                                                      --- LGGY----
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RESULT A24420

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notch

protein

fruit

fly

(Drosophila

melanogaster)

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A;Gene: notch, open A;Gene: notch, open A;Gene: notch, open A;Gross-references: FlyBase:FBgn0004647
A;Map position: 8.96-9.36
A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
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R;Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.

cell 40, 55-62, 1985

cell 40, 55-62 a novel family of transcribed repeats shared by the Notch locus
A;Reference number: A05267; MUID:85099329

A;Accession: A05267
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A; Title: Hypervariability of simple sequences as a A; Reference number: S09358; MUID:89385974
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A; Molecule type: DNA
A; Residues: 1-2703 < KID>
A; Cross-references: GB: K03508; NID: g157991; PIDN: AAA28725.1;
A; Cross-references: GB: K03508; PIDN: AAA28725.1;
A; Cross-references: GB: K03508; PIDN: AAA28725.1;
A; Cross-references: GB: K03508; PIDN: AAA28725.1;
A;
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F;2538-2568/Region:
F;2538-2568/Domain:
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A; Residues: 2504-2576, 'E', 2578-2611 <WHA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell 43, 567-581, 1985
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F;1746-1762/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: notch; opa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
475
                                                                         321
NCSQGF--TGPRCETNINECESH--PCQNEGSC-LDDPGTFRCVCMPGFTGTQCEIDIDE 529
                                                                     KCAAGFRGNGTVC-TAINACETSNGGCSTKADCKRTTPGNRVCVCKAGYTG-----DGIV
                                                                                                                                                   CHADAICDTSPINGSYACSCATGYKGVDCSEDI--DECDQGSPCEHNGICVNTP-GSYRC
                                                                                                                                                                                                                             \hbox{C-VHGRCSQGPL-GDGSCDCDVGWRGVKCDMEITTDNCN--GTCHTSANCLLDPDGKASC}
                                                                                                                                                                                                                                                                                                               ICVNGWAGL-DCSNNTDDCKQAACEYGATCIDGVGSFYCQCTKGKTGLLCHLDDACTSNP 417
                                                                                                                                                                                                                                                                                                                                                                                         MCALGTASVWDGVNGTGTCQCGLGFNGTACE-----TCTEGKYGI--HCDQACS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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EGF homology <EGF1>
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glutamine-rich
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homology <EGX3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 484;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2703;
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                                                                                      CVCQPGFV--GARCEGDINECL 1302
                                                                                                                                                                                                                                   DASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHL
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                                                                                                                                                                                                                                                                                                                                                                                                   EGITGSGECLCETGWTAASCDTPTAVFAVC-TPACSVHATCTENN---TCVCNLNYEGDG
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: A55567
R;Tilstra, D.J.; Li, Potter, K.A.; Womack, J.;
Genomics 23, 480-485, 1994
A;Title: Sequence of the coding region of the bovi.
A;Reference number: A55567; MUID:95137597
A;Accession: A55567
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2871 <TIL>
A;Cross:references: GB:L28748; NID:9508427; PIDN:A,Cross:references: GB:L28748; NID:9508427; PIDN:A,C;Superfamily: unassigned EGF-related proteins; EGF;1201-1236/Domain: EGF homology <EGF>
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                                                                                    FWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSE
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-LSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGVAYGIDCLLMNPTLGGRCDTFT:: | | | |
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Pred. No. 2.4e-21;
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OY 759 TEDIPOEC-GSCIFTPKCPLKSKPKGVKKCIYN-PLEPERRNVECCONLCTV 808 Db 1777 EIGPCVENGVCIAWNGSSFRCECKY
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	SK	862	말 .
	EPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHL-RSPLGQYKLTFD 1079	1030	Qy
c 861	DKPCEDGYYGPDCIKKCKCQGTATSSCNRVSGACHCHPGFTGEFCHALCPESTFGLKC	804	Db
C 102		987	Qу
C 803	CICPAGLEGALCTRPCSAGFWGNGCRQVCRCTSEYKQCNAQTGECSCPAGFQGDRC	748	Db
986	CVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQXGTQVSCSCKKGYKGDGYSC	932	Qy
L 747	α-	691	Db
F 931	CSEHGQCDEGI	879	Qy
s 690	ETVTPSPCASTDPKNGV	631	Db
s 878	PCNNRG-MCRDLYTPMGOCL-CHTGFNGTACE-LCWHGRFGPDCQP-RS	834	Qy
2 630	YGESCELSCPCSDASCSKQTGKCLCPLGTKGVSCDQ	595	рb
r 833	VKKKCIYNPLPFRRNVEGCQNLCTVVIQTPRCCHGYEMPDCQACPGGPDT	784	Qу
594		542	Db
3 783	LLFDVGVAYGIDCLLMNPTLGGRCDTFTTFDIPGECGSCIFTPKCPLK-SKPKG	731	Qy
5 541	GANCEKRCKCPKGIGCDPITGECTCPAGLQG	511	Db
3 730	KSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIG-ELFLNEQMCRFIHRG	672	Qy
510	RCEH	500	Db
671	AANHGYTKESKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKL	612	Qy
1 499		485	Db
611	VSISVSQDTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTV	552	Qу
484	CPLDFYGPNCAHQCQCNQRGVGCD	461	Db
551	GPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEP	492	Оу
460	DWNHASECNPETGSCVCKPGRTGKNCSE	432	рb
491	NYTEODQRICTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGP	437	Qy
431	YGADCSKTCTCVRENTLMCAPNTGFCRCKPGFYGDNCELACSKDSYGPNCEKQAMC	376	Db
436	HGG-CDRNAECTQTGPNQAVCNCLPKYTGDGKVCSLINVCLTNNGGCSPFAFC	385	Qy
375	DIGCSRGREGLOCKONCTCPGLEFSDSNASCDAKTGQCQCESGYKGPKCDERKCDAEQ	318	рb
384	GCSTKADCKRTTPGNRVCVCKAGYTGDGIVCLEINPCLEN	345	Qy
317	VGFF	258	Db
344	LDPDGKASCKCAAGFRGNGTVCTAINACETSNG	312	Qy
257	ONGGKCNKEGKCVCSDGWGGEFCLNKCEEGKFGAECKFECNCQNGATC-	210	Db
311	VH-GRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNCNGTCHTSANCL	266	Qу
209	SCSVGTWGLGCSKSCDCENGANCDPELGTCICTSGEQGERCEKPCPDNKWGPNCVKSCPC	150	Db
265	LGTASVWDGVNGTGTCQCGLGFNGTACE-TCTEGKYGIHCDQACSC	221	Qy

RESULT 12 A49175 Motch B protein - mouse (fragment) N;Alternate names: Notch homolog

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C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 20-Sep-1999
C;Accession: A49175; PH1570; S32113
R;Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety A;Reference number: A49175; MUID:93178563
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
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A:Residues: 1-1203 <LAR>
A:Residues: 1-1203 <LAR>
A:Residues: 1-1203 <LAR>
A:Residues: 1-1203 <LAR>
A:Cross-references: EMBL:X68279; NID:g287989; PIDN:CAA48340.1; PID:g287990
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBIP:126158)
C:Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C:Comment: This protein is one of the neurogenic proteins controlling the decision betwee C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
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F;560-591/Domain: EGF homology <EGF>
F:564-705/Domain: EGF homology <EGX2>
F:712-743/Domain: EGF homology <EGF3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.0%; Score 475.5; DB 2
Best Local Similarity 23.0%; Pred. No. 1.8e-21;
                                                                                                                                                                                                                                  463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 CELEVNECQSNPCVNNGQCVDKV------NRFQCLCPPGFTGP--VCQIDIDDC--SS 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 C-TAINACET----SNGGCSTKADCKRTTPGNRV-CVCKAGYTGDGIVC-LEINPCLENH 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 TDGAFHCECLKGYAGPRCEMDI ·- NECHSDPCQNDATC - LDKIGGFTCLCMPGFK -- GVH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 GDGS--CDCDVGWRGVKCDMEITTDNCNG-TCHTSANCLLDPDGKASCKCAAGFRGNGTV 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 CALGTASVWDGVNGTGTCQCGLGFNGTACETCTEGKYGIHCDQACS--CVH-GRCSQGPL 275
556 DVDECISKPCMNNGVCHNTQGSYVCECPPGFSGMDCEEDINDCLANP---
                                                        778 K----SKP---KGV-----
                                                                                                                                                                                                                                                                                                                                                                                                   617 YTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLK 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 DE---CASNPCRKGATCINDVNGFRCICPEGPHHPSCYSQVNECLSNPCIHGNCTGGLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 TPCLNGAKCID-HPNGYECQCATGFTG-----ILCDENIDNCDPDP-CHHGQCQDGI 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386 GGCDRNAECTQTGPNQAVCNCLPKYTGDGKVCSLINVCLTNNGGCSPFAFCNYTE----Q 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                     FHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVG 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHKGALCDTNPLNGQYICTCPQGYKGADCTEDVD----ECAMANSNPCEHAGKCVN---
                                                                                                                                                                    VAYGIDCLLMNPTLGGRCDTFTTFDIPGECG------SCIFTP-----KCPL 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQDTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGLNCEINFDDCASNPCMHGVCVDGINRYSCV------CSPGFTGQRCNIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSFNHEPRIKDWDQQGLMSQVL-----RYHVVGCQQLLLDNLKVTTSATTLQGEPVSISV 556
                                                                                                                 SGYTCHCML - - PYTGKNCQTVLAPCSPNPCENAAVCKEAPNFESFSCLCAPGWQGKRCTV
                                                                                                                                                                                                                            ------RCTCKKGFKGYNCQV-----NIDECASNP--C--LNQGTCFDDV 497
                                                                                                                                                                                                                                                                                                                                           Y----KCLCDAGWVGVNCE------VDKNECLSNPCQNGGTCN----NLVNGY--
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EGF homology
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                                                        ----KKKCIYNPLPFRRNVEGCQN- 804
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  606
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359	309 ARGATCDTNP1TGHWMCDCPDGWTDKDCSKDIDECSLGGNPCEHNGQCNNT :	DЬ
314	TDNCNGTCHTSANCLLDP	Qy
265 308	236 CQCGLGFNGTACETCTEG-KYGIHCDQACSC:	Оy
248	197 NGATCADAVSTYDCHCPAEWTGQYCTIDVDECSLSNNVAKRRDLQQTEGGFT	Db
235	LAHNAKPAPGEVKMCALGT ASVWDGV NGTGT	Qγ
188	135 NRCDNNDTIIVRGECGKCSQQAPCPLETKPLRETRKCIYSIYFMGKRSVFIGCQ	Оу
	atch 6.0%; Score 474.5; DB 2; Length 2352; cal Similarity 21.5%; Pred. No. 4.7e-21; 275; Conservative 97; Mismatches 440; Indels 467; Ga	Z B O
25571.1	ene: Notch	\$ 0.0 A
	coession: "30201 tatus: preliminary; translated from GB/EMBL/DDBJ olecule type: mRNA	A; A A; A
ressed in the	ori, S.; Saitoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H. . Genes Evol. 207, 371-380, 1997 itle: Notch homologue from Halocynthia roretzi is preferentially expreference number: Z20775	R; H; Dev
2000	RESULT 13 T30201 T30201 Notch homolog protein - sea squirt (Halocynthia roretzi) C;Species: Halocynthia roretzi C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-C;Accession: T30201	RESI T30 Not C; S
	1161 NCTCKAGYVG	Оу Оъ
971	1106 YHLCSAGWLESGKVAYPTTYASOKCGANVVGIVDYGSKANKSEMWDVVCYKMK-DV	ad A
915	CONGGTCIDLVNHFKCSCPPGTRGLLCEENIDECA	da
1105	ADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAK	Qy
1045 878	986 CIEIDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDCEPEOLPLDRCLQDNGQ 1 ::	Qy Db
829	777 DGAYCDYLNVSCKAAALQKGVPVEHLCQHSGICINAGNTHHCQCPLGYTG-SYC	DP CA
776	CVDGL-GTYRCICPLGYTGKNCQTLVNLCSRSPCKNKGTCVQEKARPHCLCPPGW	рр
940	85 CDEGITGSGECLCETGWTAASCDTPTAVFAVCTPA-CSVHATGTENNTCVCNLNYEG	Qγ
722	858 NGTACE	Db
662	07 GSCVDHVNTFSCQCHPGFIGDKCQTDMNECLSEPCKNGGTCSD-YVNSYTCTCPAGF) Db
857	-LCTVVIQTPRC-CHGYEMPD-CQACPGGPDTPCNNRGMCRDLYTPMGQCLCHTGF	Qy

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315 DGKASCKCAAGFRGNGTVC-TAINACETSNGGCSTKADCKRTTPGNRVCVCKAGYTGDGI 373

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В
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                    1165 KAGYVGDGFSCSGNLLQVL 1183
1174 PSGY--EGRRCQGDVNECL 1190
                                                                                                                                                                                          1052 CADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSA 1111
                                                                                                                                                    1086 CNDL-----INSYSCICALGYEGATCLTDKDECASSP---
                                                                                                                                                                                                                              1042 CLNG--GTCHDTSTA-----HECSCVAGFTGSYCD----IDIDECA--SVPCKNGAT 1085
                                                                                                                                                                                                                                                                  992 CADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDCEPEQLPLDRCLQDNGQCHPDAS 1051
                                                                                                                                                                                                                                                                                                            989
                                                                                                                                                                                                                                                                                                                                              946 TVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGD-------GYSCIEI---DP 991
                                                                                                                                                                                                                                                                                                                                                                                                                              929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             848 MGQCLCHTGFNGTACELCWHGRFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCD 907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             702 SHCDAGYTGTACEIDINECATQPCQNGGTCTSGINSYNCACPAKYTGVNCETELSPCVPN 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      427
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                                                                                                                                                                                                                                                                                                                                                                                    929 SYSCSCTANFTGDKCQNAVNNCASLQCQNGGTCYYDSGDPKCACVHGYTGTHCESLQNLC 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                               869 EEVNECASFPCKNGGICTDYVNSYVCTCLSGFYSLDCEKNIEDCSSSSCMNGGTCVDGIN 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     756 ----TFTTFDIP-----GECGSCIFTPKCPLKSKPKGVK----KKCIYN 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           643 DIQECSSNPCLHEYARRDQHVHCICDAGY-QGENCETEINECASNPCQHGACENKVAQFV 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600 ALGRVIQNLTTVAANHGYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQ 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC---ENGATCQESADYLAYVCQCPEGFRGPTCATDINEC---VNSPCKNGGGCTNL-VP 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRCGTG-----S 712
                                                                                                            GWLESGRVAYPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCYR-----MKDVNCTC 1164
                                                                                                                                                                                                                                                                                                          TGPNICK--NGG-----SCVQTSNTVSCNCLGGYEGTDCAVPQVSCTVGASLLGIAVSDL 1041
                                                                                                                                                                                                                                                                                                                                                                                                                            NNTCVCNLNYEGD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYQCTCSQGFTGKDCDTDI-----DDCSSNPCLNGGQCLDDV-GSYKCLCLPGFEGNNCQ 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLPFRRNVEGCQNLCTVVIQTPRCCHGYFMPDC----QACPGGPDTPCNNRGMCRDLYTP 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GYTGEHCDTDINECDSNPCMNGATCQNEVNNFVCQCPPGIMGTQCSS 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVGNPCQYGTCV----- 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTTSATTLQGEPVSISVSQDTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPKD 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLK 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGGCSPFAFCNYTEQDQRICTCKPDYTG-----DGIVCRGSIYGELPKNPSTSQYFFQ 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VC-----LEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKYTGDGKVCSL-INVCLTN 426
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RESULT

	Db 657INGYECVCEPGYSGSMCNINIDDCALNPCHNGGTCIDGVNSFTCLCPDGF- 706	
	Qy 559 DTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYT 618	
	QY 499 PLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQ 558 :	
	443 QRICTCKPDYTGDGIVCRGSIYGBLPKNPSTSQYFFQLQEHAVRBLAGPGPFTVFA :	
	Db 531 ASTPCKNGAKCTD-GPNKYTCECTPGESGIHCELDINECASSPCHYGYCR 579	
	QY 388CDRNAECTQTGPNQAVCNCLPKYTGDGKVCSL-INVCLTNNGGCSPFAFCNYTEQD 442	
	Qy 361 VCVCKAGYTGDGIVCLEIN	
	Qy 335AINACETSNGGCSTKADCK	
	Db 356 FFCECPHGRTGLLCHLDDACISNPCQKGSNCDTNPVSGKAICTCPPGYTGSACNQDID 413	
	-DGKASCKCAA	
	Qy 264SCVHGRCSQGPLGDGSCDCDVGWRGVKCDMEITTDNCNGTCH 305 : : :	
	Qy 232 GTGTCQCGLGFNGTACETCTEGKYGIHCDQAC 263	
	Db 199GSYLCRCPPEYTGPHCQRLYQPCLPSPCRSGGTCVQTS-D 237	···
	Oy 177 FMGKRSVFIGCOPOCVRTIITRACWLASLAHNAKPAPGEVKMCALGTASVWDGVN 231	
	Qy 135 NRCDNNDTIIVRGECGKCSQQA-PCPLETKPLRETRKCIYSIY 176	
84;	Ouery Match 6.0%; Score 473.5; DB 2; Length 2437; Best Local Similarity 20.3%; Pred. No. 5.6e-21; Matches 303; Conservative 123; Mismatches 447; Indels 617; Gaps 84	
	F:1023-1054/Domain: EGF homology <egf> F:1185-1216/Domain: EGF homology <egf2> F:1915-1947/Domain: EGF homology <egf2> F:1915-1947/Domain: ankyrin repeat homology <an1> F:1948-1980/Domain: ankyrin repeat homology <an2> F:1948-2014/Domain: ankyrin repeat homology <an3> F:2015-2047/Domain: ankyrin repeat homology <an4> F:2018-2047/Domain: ankyrin repeat homology <an5> F:2048-2080/Domain: ankyrin repeat homology <an5></an5></an5></an4></an3></an2></an1></egf2></egf2></egf>	
EGF homol	TE> MBL:X69088; NID:g433866; PIDN:CAAA8831.1; PID:g433867 gned ankyrin repeat proteins; ankyrin repeat homology; homology <egf1></egf1>	
its patter	C.; Campos-Ortega, J.A. 3, 87-100, 1993 ebrafish homologue of the Drosophila neurogenic gene Notch and number: S42612; MUID:94128602 S42612	
	transmembrane protein precursor - zebra fish C:Species: Brachydanio rerio (zebra fish) C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Sep-1999 C:Accession: S42612	

90;

RESULT 15 T13954 MEGF6 protein - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 C;Accession: T13954 R;Nakayama, M; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O. Genomics 51, 27-34, 1998 A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs A;Reference number: Z14126; MUID:98360089 A;Accession: T13954 A;Scession: T13954 A;Scatus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Cross-references: EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3449294 A;Experimental source: strain Sprague-Dawley; brain	QY 1129 KCGANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGYVGDGFSCSGNLLQVLM 1184	Qy 972SCSCKKGYKGDGYSC-IEIDPCADGVNGG-CHEHATCRMTGPGKH 1014	Qy 874 -CQPRSCSEHGQCDEGITGSGEC 895 l <	821 MPDCQACPGG	Qy 726 FIHRGLLEDVGVAYGIDCLLMNPTLGGRCDTFTTFDIPGECGSCIFTPKC 775	OY 619 KFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQODFLFNQDNKDKLKSYL 675
Qy 717 LFLNEOMCRFIHRGLLFDVGVAYGIDCLLMNPTLGGRCDTFT 758	QY 606 QNLTTVAANHGYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLF 663	Oy 458 VCRGSIYGELP	OY 305 HTSANCLLDPDGKASCKCAAGERGNGTVCTAINACETSNGGCSTKADCKRTTP 357	231 NGTGTCQCGLGFNGTACETCTEGKYGIHCDQACSCVHGRCS	Qy 152 CSQQAPCPLETKPLRETRKCIY	C;Genetics: A;Gene: MEGF6 A;Gene: MEGF6 Ouery Match Best Local Similarity 22.4%; Pred. No. 3.5e-21; Matches 300; Conservative 99; Mismatches 460; Indels 478; Gaps

Db	Оу	Db	Qy	DЪ	ОУ	DЬ	Qy	DЬ	Qy	DЬ	Qy	Db
Db 1233 PASGV-CTCAAGYHGTG 1248	Oy 1156 RMKDVNCTCKAGYVGDG 1172	Db 1175 CAQRCLCPTNASCHHVTGECRCPPGFTGLSCEQACQPGTFGKDCEHLCQCPGETWACD 1232	Qy 1118RVAYPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCY 1155	Db 1115 TGDKCQSSCVSGTFGVHCEEHCACRKGASCHHVTGACFCPPGWRGPHCEQACPRGWFGEA 1174	1077]	Db 1070 GWTGLACENECLPGHYAAGCQLNCSCLHGGICDRLTGHCLCPAGW	1021 HYVGDGVDCEP	Db 1021QCHCAPGWMGPTCLQACPPGLYGKNCQHSCLCRNGGRCDPILGQCTCPE 1069	965 SQKGTQVSCSCKKGYKGDGYSCIEIDPO	Db 963 ACNCSAGAPCDAVTGSCICPAGRWGPRCAQSCPPLTFGLNCSQICTC-FNGASCDSVTG- 1020		Db 906 QSCRQGYYGPSCEQKCRCEHGAACDHVSGACTCPAGWRGSFCEHACPAGFFGLDCDS 962
		KDCEHLCQCPGETWACD 12	SRANKSEMWDVFCY 11	GWRGPHCEQACPRGWFGEA 11	LCSAGWLESG 1117	CDRLTGHCLCPAGW 1114	QDTTVGVFHLRSPLGQYKL 10	CRNGGRCDPILGQCTCPE 10	TCRMTGPGKHKCECKS 1020	SQICTC-FNGASCDSVTG- 10	TVVDFCKQNNGGCAKVAKC 964	: : : GSFCEHACPAGFFGLDCDS 96
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Search completed: June 17, 2002, 12:31:15 Job time: 281 sec

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Q90yd2 xenopus lae	3 Q90YD2		1214	5.2	406	45
Q90819 gallus gall		13	1193	5.2	410	44
a	o		1722	5.2	411.5	43
	Q21281	ഗ	2104	5.3	413.5	42
Q9vb65 drosophila	Q9VB65	U	1404	5.3	414.5	41
Q90y57 brachydanio	3 Q90Y57	13	1242	ω	415	40
Q96jp8 homo sapien	Q96JP8	4	2809	5 .ω	420.5	39
035452 mus musculu	035452	1	4006	5.4	421	38
Q964n4 caenorhabdi	Q964N4	ű	2104	5.4	423.5	37
	Q96KG7	4	1140	5.4	424.5	36
Q9npk9 homo sapien	Q9NPK9	4	4288	5.5	430	35 5
Q9vm55 drosophila	Q9VM55	G	3396	ა. ა	431	34
	Q96KG6	4	969	5.5	431	33
	018977	6	4135	5.5	434	32
035442 mus musculu			1964	5.6	437.5	31
013149 fugu rubrip		13	2447	5.6	443	30
			2319	5.7	447	29
Þ	Q9H240	4	2471	5.7	450.5	28
	004721	4	2471	5.7	450.5	27
	016004	ű	2531	5.7	452	26
	Q9VR08	Ŋ	3680	5. 8	453.5	25
000306 homo sapien	000306	4	2003	5. 8	459.5	24
Q99940 homo sapien	099940	4	1999	5.9	461.5	23
Q9qw30 rattus sp.,	Q9QW30	11	2471	5.9	465	22
Q9um47 homo sapien	Q9UM47	4	2321	6.0	469	21
Q9y618 homo sapien	0916L8	4	2321	6.0	469	20
Q9upl3 homo sapien	Q9UPL3	4	2281	6.0	469	19
088281 rattus norv	. 088281	11	1574	6.0	473	18
061240 halocynthia	061240	σ	2352	6.0	474.5	17

ALIGNMENTS

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pfam; pF00008; EGF; 9.
pfam; pF00008; EGF; 9.
pfam; pF002469; Fasciclin; 2.
pfam; pF00193; XIINK; 1.
pRINTS; pR00191; EGFLAMININ.
pRINTS; pR01265; LINK; 1.
proDom; pD000918; Link; 1.
SMART; SM00481; EGF; 9.
SMART; SM00481; LINK; 1.
pR0SITE; pS00022; EGF_1; UNKNOWN_1.
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O9H7H7;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-DEC-2001 (TrEMBLrel. 16, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FLJ00112 PROTEIN (FRAGMENT).
FLJ00112.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                              InterPro; IPR000782; BIgH3_fasciclin.
InterPro; IPR000561; EGF-like.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR000538; Link.
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"The nucleotide sequence of a long cDNA clone isolated from human
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SFYNDLVNGTFLRTMLGSQLLITFSQDQLH-QETRFVDGRSILQWDIIAANGILHIISEP
                                    GSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTCKVGYVGDGFSCSGNLLQVLMSFPSLT
                                                                                 GANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGYVGDGFSCSGNLLQVLMSFPSLT
|: |||||||||
                                                                                                                               LGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYASQKC
                     NFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLANVSM
                                                                                                                                                                                                                        CKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIEIDPCADGVNGGCHEHATCRMTG
                                                                                                                                                                PGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSP 846
                                                                                                                                                                                                             CKQDNGGCAKVARCSQKGTKVSCSCQKGYKGDGHSCTEIDPCADGLNGGCHEHATCKMTG
                                                                                                                                                                                                                                                                     GSGECLCETGWTAASCDTPTAVFAVCTPACSVHATCTENNTCVCNLNYEGDGITCTVVDF
                                                                                                                  LGQYKLTFDKAREACANEAATMATYNQLSYAQKAKYHLCSAGWLETGRVAYPTAFASQNC
                                                                                                                                                                            PGKHKCECKSHYVGDGVDCEPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHLRSP 1070
                                                                                                                                                                                                                                                          GSGQCLCETGWTGPSCDTQAVLPAVCTPPCSAHATCKENNTCECNLDYEGDGITCTVVDF
                                                                                                                                                                                                                                                                                                                  PDTPCNNRGMCRDLYTPMGQCLCHTGFNGTACELCWHGRFGPDCQPRSCSEHGQCDEGIT
                                                                                                                                                                                                                                                                                                                                                                                                  PDAPCNNRGVCLDQYSATGECKCNTGFNGTACEMCWPGRFGPDCLPCGCSDHGQCDDGIT
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                                                                                                                                                                                                                                                                                                                                                                 FTPKCPLKSKPKGVKKKCIYNPLPFRRNVEGCQNLCTVVIQTPRCCHGYFMPDCQACPGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOLLLENLKLISNATSLQGEPIVISVSQSTVYINNKAKIISSDIISTNGIVHIIDKLLSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGTGVCECGEGFSGTACETCTEGKYGIHCDQACSCVHGRCNQGPLGDGSCDCDVGWRGVH
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77.7%;
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Pred. No. 0;
05; Mismatches
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Best Local Similarity 73.1%;
Matches 798; Conservative 100
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PRINTS; PRO1265; LINKKODULE.

PRODOM; PD000918; Link; 1.

SMART; SM00181; EGF; 8.

SMART; SM00445; LINK; 1.

PROSITE; PS001022; EGF_1; UNKNOWN_2.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01148; LAMININ_TYPE_EGF; 1.

EGF-1ike domain; Glycoprotein; Hypothetical procession of the property o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00008; EGF; 8. Pfam; PF02469; Fasciclin; 2. Pfam; PF00193; Xlink; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 115.7 KDA PROTEIN (FRAGMENT).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1147
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InterPro; IPR000561; EGF-like.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR000538; Link.
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VFAPLSAAFDEBARVKDWDKYGLMPQVLRYHVVACHQLLLENLKLISNATSLQGEPIVIS
                                    VFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSIS
                                                                                                                                                                                                                                                                                                               LEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKYTGDGKVCSLINVCLTNNGGCSPPAF 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKASCKCAAGERGNGTVCTAINACETSNGGCSTKADCKRTTPGNRVCVCKAGYTGDGIVC 375
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100; Mismatches
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CD44-LIKE PRECURSOR FELL.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                       O9NRY3; PRELIMINARY;
Q9NRY3;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                              QDQLH-QETRFVDGRSILQWDIIAANGILHIISEPLRAPPTAATAAHSGLGTGIFCAVVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKGYKGDGYSCIEIDPCADGVNGGCHEHATCRMTGPGKHKCECKSHYVGDGVDCEPEQLP
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                                                                                                                                                                                  HPQSPPVTPSQ 1399
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                                                                                                                                                                                                                                                   QDPLQPTETRFVDGRAILQWDIFASNGIIHVISRPLKAPPAPVTLTHTGLGAGIFFAIIL
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             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Matches 676
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Pfam; PF02493; Xlink; 1.

PFINTS; PR01265; LINKMODULE.

PRODOm; PD000918; Link; 1.

SMART; SM00481; EGF; 5.

SMART; SM00445; LINK; 1.

PROSITE; PS00122; EGF_1; UNKNOWN_2.

PROSITE; PS01186; EGF_2; 4.

PROSITE; PS01248; LAMININ_TYPE_EGF; 1.

EGF-11ke domain; Glycoprotein; Laminin EG
SEQUENCE 897 AA; 97585 MW; EB920AF361
                   1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1999) to the EMBL; AF160476; AAF82398.1; HSSP; P98066; ITSG.
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Tao Q., Zhang W., Cao )
"Molecular cloning and
with CD44.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000782; BIgH3_fasciclin
InterPro; IPR000561; EGF-like.
InterPro; IPR002049; Laminin_EGF.
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                                      VAYPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGYVGDGFSCSGN
                                                                                                                              EGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIEIDPCADGVNG
                                                                                                                                                                      CSEHGOCDEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVHATCTENNTCVCNLNY
                                                                                                                                                                                                                                           TFDASGECGSCVNTPSCPRWSKPKGVKQKCLYN-LPFKRNLEGCRERCSLVIQIPRCCKG
                                                                                                                                                                                                                                                      TFDIPGECGSCIFTPKCPLKSKPKGVKKKCIYNPLPFRRNVEGCQNLCTVVIQTPRCCHG
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676; Conserv
VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTCKVGYVGDGFSCSGN
                                                                                                                     EGDGITCTVVDFCKQDNGGCAKVARCSQKGTKVSCSCQKGYKGDGHSCTEIDPCADGLNG
                                                                                                                                                            CSDHGQCDDGITGSGQCLCETGWTGPSCDTQAVLPAVCTPPCSAHATCKENNTCECNLDY
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76.18;
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Pred. No. 0;
87; Mismatches
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EB920AF36101E388
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PROSITE;
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SMART; SM00180; EGF_Ltam; 1.
SMART; SM00001; EGF_Like; 13.
SMART; SM00445; LINK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97191544; PubMed=9039502;
Magase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara Tanaka A., Kotani H., Miyajima N., Nomura N.;
Tanaka A., Kotani H., Miyajima N., Nomura N.;
"Prediction of the coding sequences of unidentified human genes.
"the coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced analysis of cDNA clones from cell line KG-1 and brain.";
DNA Res. 3:321-329(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pfam; PF00008; EGF; 13.
pfam; PF02469; Fasciclin; 3.
pfam; PF00193; Xlink; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR000782; BIGH3_fasciclin.
Interpro; IPR001128; Cyt_P450.
Interpro; IPR000561; EGF-like.
Interpro; IPR0002049; Laminin_EGF.
Interpro; IPR000538; Link.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
KIAA0246 PROTEIN (FRAGMENT)).
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                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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AANGILHIISEPLRAPPTAATAAHSGLGTGIFCAVVLVTGAIALAAYSYFRLKQRTTGFQ
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                                                                                                                                                                                                                                                                                                domain; Glycoprotein; Laminin
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EGF_2; 13.
LAMININ_TYPE_EGF;
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No. 1e-229;
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                               PDASCADLYFODTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYH
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                                                                                                                                                           NNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIE
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                                                                   RNPCTDGHRGGCSEHANCLSTGLNTRRCECHAGYVGDGLQCLEESEPPVDRCLGQPPPCH
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R Pfam: pF00193; Xlink; 1.

R PRINTS; PR00011; EGFLAMININ.

PP0Dom; PD000918; Link; 1.

R SMART; SM00101; EGF-Link; 1.

R SMART; SM00001; EGF-Link; 15.

R SMART; SM00001; EGF-Link; 15.

R SMART; SM00001; EGF-Link; 1.

R PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_2.

R PROSITE; PS00128; EGF-1; UNKNOWN_7.

R PROSITE; PS01186; EGF-2; 16.

R PROSITE; PS01248; LAMININ_TYPE_EGF; 2.

R PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
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Best Local Similarity 40.0%; P
Matches 561; Conservative 222;
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Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
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   LLQQLDLVPAFSLFRELLQHHGLVPQIEAATAYTIFVPTNRSLE---AQGNSSHLDADTV 1187
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P98066; 1TSG.
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IPR001128; Cyt_P450.
IPR000561; EGF-like.
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(TrEMBLrel. 19, Last annotation updat
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                                                                                         NNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIE
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LCSAGWLESGRVAYPTTYASQKCGANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAG
                                                 PDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYH
                                                                                                                                                          \tt GNSCECSLGYEGDGRYCTVADLCQDGHGGCSEHANCSQVGTMVTCTCLPDYEGDGWSCRA
                                                                                                                                                                                                                         AFGPHCQACRCTVHGRCDEGLGGSGSCFCDEGWTGPRCEVQLELQPVCTPPCAPEAVCRA
                                                                                                                                                                                                                                         RFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVHATCTE
                                                                                                                                                                                                                                                                                        {\tt TTWKPSCCPGHYGSECQACPGGPSSPCSDRGVCMDGMSGSGQCLCRSGFAGTACELCAPG}
                                                                                                                                                                                                                                                                                                   VIQTPRCCHGYFMPDCQACPGGPDTPCNNRGMCRDLYTPMGQCLCHTGFNGTACELCWHG
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                               SDAMCTDQHFQEKRAGVFHLQATSGPYGLNFSEAEAACEAQGAVLASFPQLSAAQQLGFH
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Best Local Similarity
Matches 296; Conserv
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InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR000884; TSP1.
Pfam; PF00008; EGF; 24.
SMART; SM00101; EGF; 30.
SMART; SM00101; ASX_HYDROXYL; 22.
PROSITE; PS00101; ASX_HYDROXYL; 22.
PROSITE; PS01186; EGF_CA; 18.
PROSITE; PS01187; EGF_CA; 18.
PROSITE; PS01187; EGF_CA; 18.
Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SEQUENCE 2189 AA; 224388 MW; C272A420B94FCB2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1338
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Tomley F.M., Billington K.J., Bumstead J.M., Clark J.D., Monaghan P.;
"EtMIC4: A microneme protein from Eimeria tenella that contains tandem arrays of epidermal growth factor-like and thrombospondin type-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9BI05 PRELIMINARY; PRT; 2189 AA.
Q9BI05;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MICRONEME PROTEIN 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeats.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJJ06453; CAC34726.1; -.
HSSP; P35555; 1EMN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
Eimeria.
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   543
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                                                                239
                                                                                                                             516
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                                                                                                                                                                                                                                                    MEGNACSDID-----ECSEASTEIPENCNCVNTEGSFSLEAKPGYELVDGKCV-KIDF- 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSGLPGNKSLSGRDIEHHLTNVNVSFYNDLVNGTFLRTMLGSQLLITFSQDQLHQETRFV 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FVGDGISTCNGKLLDVLAATANFSTFYGMLLGYANATQRGLDFLDDELTYKTLFVPV 2372
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   GYSGDGTA----QG---
                                                             GLGFNGTACETCTEGKYGIHCDQACSCV------HGRCSQGPLGDGSCDCDVGWR--
                                                                                                                          ------CAR----GAC--NSLAHCKENPEGTAAIC-----TCIA 542
                                                                                                                                                                                    GKRSVFIGCQPQCVRTIITRACWLASLAHNAKPAPGEVKMCALGTASVWDGVNGTGTCQC 238
                                                                                                                                                                                                                                                                                                                                                                        7.7%; Score 603.5; DB 5; Length 2189; ilarity 24.3%; Pred. No. 2.3e-41; Conservative 114; Mismatches 459; Indels 347; Gaps
HCDDIDECLAENDCTPADQGGICENTVGSYTCKCAAGYQQD
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	SCPGVDNNLSHRRAE 1437	1422	Db Vy
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GTLFVPQN 1227 : : ACGELGEW 1421	CSGN-LLQVLMSFPSE/MELTEVLAFSKSSARGQAFLKHLTDLSIRGTLFVFOU : :	1175	Dh Qy
13	AGNHAGDINAVC	1326	Db
VGDGFS 1174	ASQKCGANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGYVGDGFS	1126	Qy
CEDV 1325	GYEMKDGACVDIDECQSGTHNCDPHADCSNTDGSFTCTCGSGYTGVGTLCEDV	1273	Db
AYPTTY 1125	GQYKLTFDKAKEACAK-EAATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTY	1072	Qу
: NCTCKA 1272	GSHTCTCNEGYQGDGKKCEKTVGPC-DNSPCGNNAMCEATADSYNCTCKA	1224	Db
HLRSPL 1071	GKHKCECKSHYVGDGVDCEPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHLRSPL	1012	Qy
CTNT-E 1223	AAGTATCGERSFCVDTQGSYKCECKNGYRQCGEDCVDVDECEADVH-TCSEHATCTNT-	1166	Db
CRMTGP 1011	KQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSCIEIDPCADGVNGGCHEHATCRMTG	952	Qу
DNVDEC 1165	FSGDG-HTCTDIDECADPNLNKCDTHKGICQNGTGSYTCGCRPGYSLAADGFTCDNVDEC	1107	Db
IVVDFC 951	WTAASCDTPTAVEAVCTPACSVHATCTENNTCVCNLNYEGDGTTCTVVDEC	901	Qy
CGCKEG 1106	F-TCSCAAGFTGDGLTCEDIDECATAAH-TCDPNATCVNTVGSFECGCKEG	1058	Db
GSGECLCETG 900	MGQCLCHTGFGTACELCWHGREGPDCQPRSCSEHGQCDEGITGSGEC	848	Qy
rntvgs 1057	CTCQDIDECLDGK-MNTCAPVGGICTNTVGS	1028	Db
RDLYTP 847	CIYNPLPFRRNVEGCQNLCTVVIQTPRCCHGYFMPDCQACPGGPDTPCNNRGMCRDLYTP	788	Оу
SFIKRR 1027	ECSVGEPCKDFGEGGVCVDSPGSFSCSCATGFIKRR	992	dd
3-VKKK 787	RGLLFDVGVAYGIDCLLMNPTLGGRCDTFTTFDIPGECGSCIFTPKCPLKSKPKG-VKKK	729	Qу
-GEEGCKNID 991	KIDFCSEKGCNANASCKENDAGTEAICTCHSGYEGNGEGEEG	945	Дb
MCRFIH 728	KLKSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSD-IGELFLNEQMCRFIH	670	Qy
GYRHTENGCT 944	QQDGAVGCIDIDECAASTAVLPANATCVNTEGSYTFECVPGYRHT	895	Db
NODNKD 669	KFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKD	619	Qy
GYT 894	GFQGDGHSCTDIDECATOGVCGEHATCENTAGSYNCTCEA-	852	Db
ANHGYT 618	KVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYT	568	Qy
ECSCLP 851	EGFVAVGAKLKGATSLTCIDIDECNDASKNTCATSADGGSCKNTAGSYECSC	798	Db
567	LRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEA	523	Оy
CACV 797	-HGENGCQDIDECAQDAICGENTVCTNTPGSFE	762	Db
SLMSQV 522	IYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQV	463	Оy
761	CECNPSFDGDGHKCEDVDFCGQGLHDCNVHAECSESDDNTTFKCTCGIGYTGEG-	708	dd
IVCRGS 462	CNCLPKYTGDGKVCSLINVCLTNNGGCSPFAFCNYTEQDQRI-CTCKPDYTGDGIVCRGS	404	Оу
4-GSFT 707	DCGENTLCNNTV-GSFECTCMAGFEAADAKTCKDIDECASGTHTCSTHATCTNTA-	650	Db
SPNQAV 403	GCSTKADCKRTTPGNRVCVCKAGY-TGDGIVCLEINPCLENHGGCDRNAECTQTGPNQAV	345	Оу
CSTDAD 649	GNSCTDIDECANGTHNCHASATC-TNTQGSFECACNAGFSGNGVECNDVDECSTDAD	594	Db
CETSNG 344	GVKCDMEITTDNC-NGTCHTSANCLLDPDGKASCKCAAGFRGNGTVCTAINACETSNG	288	Qy

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Best Local Similarity
Matches 296; Conserv
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Pfam; PF00083; TB; 12.

SMART; SM00494; ChtBD2; 2.

SMART; SM00179; EGF_1ike; 4.

SMART; SM001019; EGF_1ike; 4.

PROSITE; PS00010; ASX_HYDROXYL; 61.

PROSITE; PS00018; EGF_1; UNKNOWN_2.

PROSITE; PS01186; EGF_2; 50.

PROSITE; PS01187; EGF_CA; 61.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.

Calcium-binding; EGF-1ike domain; Glycoprotein; Hydroxylation; SECUENCE 3857 AA; 418301 MW; 5BC0618BC527E04C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-DEC-2001 (TrEMBLrel. 19, MUTANT FIBRILLIN-1.
     1426
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InterPro; IPR002557; Chitin_binding.
InterPro; IPR000561; EGF-Like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR002212; TB.
InterPro; IPR000822; Znf-C2H2.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 4:267-271(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure of the mutant fibrillin-1 gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsuda F
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                                   399
PGGYRCECDMGFVP--SADGKACEDIDECSLPNICVFGTCHNLPGLFRCECEIGYELDRS 1483
                          PNQAVCNC----LPKYTGDGKV-----CSLINVCL-----
                                                                                                                                                                                                                                                                                                                                                         IQKNRCDNNDTITVRGEC----GKCSQQAPCPLETKPLRETRKCI----YSIYFMG----
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                                                                                                                             KKGKTGCTDINECEIGAHNCGRHAVCTNTA-----GSFKCSCSPGWIGDGIKCTDLDE
                                                                                                                                                                                               PGEYRCLCYDGFMASEDMKTCVDVN---ECDLNPNICLSGTC-ENTKGSFICHCDMGYSG
                                                                                                                                                                                                                NGTGTCQCGLGFNGTA-CETCTEGKYGIHCD-QACSCVHGRCSQGPLGDGSCDCDVGWRG
                                                                                                                                                                                                                                                           CTNSDGSYECSCQPGFALMPDQRSC-----TDIDECE-DNPNICDGGQCTNI 1259
                                                                                                                                                                                                                                                                                           ----KRSVFIGCQPQCVRTIITRACWLASLAHNAKPAPGEVKMCALGTASVWDG-----V
                                                              CSNGTHMCSQHADCKNTM-GSYRCLCKDGYTGDGFTCTDLDECSENLNLCG-NGQCL-NA
                                                                                CETSNGGCSTKADCKRTTPGNRVCVCKAGYTGDGIVCLEINPCLENHGGCDRNAECTQTG
                                                                                                                                                                                                                                                                                                                         IDINECELSANLCPHGRCVNLIGK--YQCACNPGYHPTHDRLFCVDIDECSIMNGGCETF
                                                                                                                                                             VK----C----DMEITTDNC--NGTCHTSANCLLDPDGKASCKCAAGFRGNGTVCTAINA 338
                                                                                                                                                                                                                                                                                                                                                                                      7.1%; Score 557; DB 11; Length 3857; ilarity 20.6%; Pred. No. 5e-37; Conservative 136; Mismatches 403; Indels 600;
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                               426
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Oy 1035 PLDRCLQDNGOCHPDASCADLYFQDTTYGYFHLRSPLGQYKLTFDKAKERC 1085 Db 2432 DIDECSLPNICVFGTCHNLPGLFRCECEIG-YELDRSGGNC 2471	
	,
2383 GDGFTCTDLDECSENINLCGNGQCLNAPGGYRCECDMGFVPSADGKACE 2	
NGGCH	0
Db 2325 CTNTAGSFKCSCSPGWIGDGIKCTDLDECSSGTHMCSQHADCKNTMGSYRCLCKDGYT 2382	н
ENNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVSCSCKK	0
Db 2265 VDVNECDLNPNICLSGTCENTKGSFICHCDMGYSGKKGKTGCTDINECEIGAHNCDRHAV 2324	н
Qy 905CSCDTPTAVFAVCTPACSVHAT 925	_
Db 2205 YECSCQPGFALMPDQRSCTDIDECEDNPNICDGGQCTNIPGEYRCLCYDGFMASEDMKTC 2264	_
Qy 870 FGPDCQPRSCSEHGQCDEGITGSGECLCETGWTAA 904	_
Db 2145 CELSANLCPHGRCVNLIGKYQCACNPGYHPTHDRLFCVDIDECSIMNGGCETFCTNSDGS 2204	н
Qy 845ACE-LCWHGR 869	_
Db 2088 ESGFMMMKNCMDIDECQRDPLLCRGGICHNTEGSYRCECPPGHQLSPNISACIDINE 2144	_
Qy 820FMPDCQACPGGPDTPCNNR	_
Db 2028 GKCRNTIGSFKCRCDSGFALDSEERNCTDIDECRISPDLCGRGQCVNTPGDFECKCDEGY 2087	m
Qy 808VVIQTPRCCHGY 819	0
Db 1968 CSVGAAWGTEECEECPLRNSREYEELCPRGPGFATKDITNGKPFFKDINECKMIPSLCTH 2027	н
KPKGVKKKC	_
Db 1908 KNGLCVNSRGSFKCECPNGMTLDATGRICLDIRLETCFLKYDDEECTLPIAGRHRMDACC 1967	r=4
Qy 767GSCIFT 772	0
Db 1861 CCSSLGAAWGSPCTICQLDPICGKGFSRIKGTQCEDINECEVFPGVC 1907	_
Qy 723 MCRFIHRGLLFDVGVAYGIDCLLMNPTLGGRCDTFTTFDIPGEC 766	_
Db 1807 CKNSPGSFICECSPESTLDPTKTICIETIKGTCWQTVIDGRCEININGATLKSE 1860	_
KLKSYLKFHVIRDSKALASDLPRSASW	_
Db 1759SLCDNGQCRNTPGSFVCTCPKGFVYKPDLKTCEDIDECESSPCINGV 1806	-
Qy 616 GYTKFSKLIQDSGLLSVITDSTHTPVTVFWPTDKALEALPPEQQDFLFNQD 666	_
Db 1711 NEC-ALDPD-ICPNGICENLRGTYKCICNSGYEVDITGKNCVDINECVLN- 1758	
Qy 565 NEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANH 615	_
Db 1656 TPGICGPGTCYNTVGNVTCICPPDYMQVNGGNNCMAEYQALCSSG-PGMTSAGTDI 1710	п
Qy 515 QQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFIN 564	0
Db 1598 RPNPITVILEDIDECQELPGLCQGGKCINTFGSFQCRCPTGYYLNEDTRVCDDVNECE 1655	_
Qy 477FFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKDWD 514	_
Db 1538 LDIRPRGDNGDTACSNEIGVGVSKASCCCSLGKAWGTPCELCPSVNTSEYKILCPGGEGF 1597	н
Qγ 465 476	\sim
Db 1484 GGNCTDVNECLDPTTCISGNCVNTPGSYTCDCPPDFELNPTRVGCVDTCSGNCY 1537	н
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R Interpro; IPR0001561; EGF-1ike.

R Interpro; IPR000742; EGF_2.

R Interpro; IPR001881; EGF_Ca.

R Interpro; IPR001881; EGF_Ca.

R Interpro; IPR001881; EGF_Ca.

R Interpro; IPR001491; Thrmbomoduln.

R Interpro; IPR001491; Thrmbomoduln.

R Pfam; PF00008; EGF; 19.

R PRINTS; PR00907; THRMBOMODULN.

R PRINTS; SM001181; EGF; 19.

R PROSITE; SM00101; ASX_HYDROXYL; 14.

R PROSITE; PS00100; ASX_HYDROXYL; 14.

R PROSITE; PS00100; ASX_HYDROXYL; 14.

R PROSITE; PS001186; EGF_1; UNKNOWN_1.

R PROSITE; PS01186; EGF_2; 19.

R PROSITE; PS01187; EGF_CA; 12.

R PRO
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Best Local Similarity 20.4
Matches 212; Conservative
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MEDLINE=21347414; PubMed=1145543;
Nakayama A., Satou Y., Satoh N.;
"Isolation and characterization of genes the Ciona intestinalis metamorphosis.";
Dev. Genes Evol. 211:184-189(2001).
EMBL; AB041857; BAB40596.1;
HSSP; P00742; 1HCG.
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Q9BLJ1;
Q9BLJ1;
01-JUN-2001 (TrEMBLrel. 1:
01-JUN-2001 (TrEMBLrel. 1:
01-DEC-2001 (TrEMBLrel. 1:
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Eukaryota; Metazoa; Chordata; Urochordata;
Cionidae; Ciona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7719;
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                                                                                                                                                                                                                                                                                                                             PCLENHGGCDRNAECTQTGPNQAVCNCLPKYTGDGKVCSLINVCLTNNGGCSPFAFCNYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGFRGNGTVCTAINACETSNGGCSTKADCKR--TTPGNRVCVCKAGYTGDGIVCLEIN 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACWLASLAHNAKPAPGEVKMCA------LGTASVWDGVNGTGTCQCGLGFNG-----
                                                                   LSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQD
                                                                                                                                                                                                                                                                                        EC--RSSPCGNNAQCINT-PGSFTCRCNTGYTGNGRICRDVNECAAIRPPCSPNADCTNT
                                                                                                                                                                                                                                                                                                                                                                                                                                          CKPGYRAQGSRCVDINECLRPN-VCGPASHNKRCVNTPGSFRCVCRNGYRAQGSRCVDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKRCVNTAGSFRCVCKNGYRAQGSRC---VDINECLRPNICGINSNKRCVNRPGG-YRCV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTAIDPCNPSPCGAHA--TCSSVHYRPVCTCEAGYTGNPQTGCTDVNECLRPNVCGPASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -TACETCTEGKYGIHCDQACSCVHGR----CSQGPLGD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCFNAAQPNNQRCRNYKIRFCCPNDPCNPSPCGAYATCSNVHYRPVCTCNAGYTGNPQTG
                                                                                                                                                                               EQDQRICTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GS--CDCDVGWR--GVKCDMEITTDNC--NGTCHTSAN--CLLDPDGKASCK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.1%; Score 555.5; DB 5; 20.4%; Pred. No. 7.3e-38; rative 88; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17,
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Mortimore B.; Gibeithod (App-1000) to the GMDI (Coppe, VDDBI database)	RA:
SEQUENCE F	R R To N
NCBI_TaxID=6239;	0.0
Eukaryota; Me Rhabditidae:	2 8
Caenorhabditis elegans.	80
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01-DEC-2001 (TremBLrel. 19, Last annotation upda	201
01-MAY-2000 (Tremblrel, 13, Created)	
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TVQ2 OGTVO2 DRF: IMINARY: DRT	7 P.E.
746 -CRAVNYRPVO	Db
1156 RMKDVNCTCKAGYVG	Qy
b 718 CNRGYTGNGRVCFPVNPCSPSPCGSNAI 745	Db
1097 QLSYAQKAKYHLCSAGWLESGRVAYPTTYAS-QKCGANVVGIVDYGSRANKSEMWDVFCY 11	Qy
693 NEC-NNPRACHPQATCANT	Db
1037 DRCLQDNGQCHPDASCADLYFQDTTVGVFHLF	Qy
639 IGYRKVRGNCVDINECR-ASRRPCDLNASCQNT-PGSETCTCN	Db
977 K	Qy
580 CSPNADCTN	Db
920 CSVHATCTENNTCVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTC	Qy
538	DЬ
860 TACELCWHGRFGPDCQPRSCSEHGQCDEGITGSGECLCETGWTA	Qy
514TC	Db
800 EGCQNLCTVVIQTPRCCHGYFMPDCQACPGGPDTPCNNRGMCRDLYTPMG	Qy
486 GSRCVDINECRSSPCGNNARCINT	Db
740 GIDCLLMNPTLGGRCDTFTTFDIPGECGSCIFTPKCPLKSKPKGVKK	Qy
b 473VCRNGYRAQ 485	Db
680 IRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFI	Qy
b 473 472	Db
y 620 FSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHV 679	Qy
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Best Local Similarity
Matches 305; Conserv
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EMBL: AL110498; CAB60454.1; JOINED.
EMBL: AL110498; CAB57911.1; -.
EMBL: AL117206; CAB57911.1; JOINED.
HSSP: P00736; 1APQ.
InterPro; IPR000152; Asx. hydroxyl.
InterPro; IPR000152; Asx. hydroxyl.
InterPro; IPR001881; EGF-1ke.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR002049; Laminin_EGF.
Pfan: PF00008; EGF; 25.
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SMART; SM00179; EGF_CA; 4.

SMART; SM00001; EGF_1ike; 18.

PROSITE; PS00010; ASX_HYDROXYL; 4.

PROSITE; PS00102; EGF_1; UNKNOWN_22.

PROSITE; PS01186; EGF_2; 24.

PROSITE; PS01186; EGF_2; 24.

PROSITE; PS01187; EGF_CA; 3.

Calcium-binding; EGF-11ke domain; Glycoprotein; Hydroxylation; Repeat.

SEQUENCE 1664 AA; 179279 MW; A69F093B4C705832 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      323
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544 VFGRRRHVKACVNFQGTLSLELFSSEVRTD-----PSEKCPNGF----
                                                                                                                                                                                                                          433
                                                                                                                                                                                                                                                                                                                            381 CLENHGGCDRNAECTQTGPNQA----VCNCLP---KYTGDGKVCSLINVCLTNNGGCSPFAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 TIGTYYCRCWPGFELSGDGNTCSDIDECAVSNGGCSDRCVNSPGGFRCDCPSDLYLHADG 193
                                                                                                                                                                                                                                                                                            381 CHENNG-----DCSQICVNLAGSVECQCKPGFRLMKDRKTCEDISECSSNNGGCE--QI 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 VLEIQKNRC-----CPLETKPLRET 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 CHNG---GTCVPSEH-----NDNEQVCECPVGFTGAKCQYDANECMANNGGCEHECVN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 IFFRELGEIEKLD----FLPFNFHARKYLRFARFSRRGCS-KCCLLRVQANCSADL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 IHYNLASAIESADAYTVFVPNNEAIENYIR----EKKATSLKEDILRYHVVLGEKLLKND 78
                                                                                                                                                                                                                                          CNYTEQDQRICTCKPDY--TGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRE-LAGPG 492
                                                                                                                                                                                                                                                                                                                                                                   YQLGRDGRTCEEMLGGCQVGNGGC--QHDCYDQPDGGHVCKCRNGYILANDQKLCHDINE
                                                                                                                                                                                                                                                                                                                                                                                          FR--GNGTVC-TAINACETSNGGCSTKADCKRTTPGNRVCVCKAGY--TGDGIVCLEINP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQGPLGDGSCDCDVGWRGVKCDME--ITTDNC---NGTCHTSANCLLDPDGKASCKCAAG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHNGMHRETMLGFSYLLAFFLRNDQLYVNEAPINYTN-----VATDKGVIHGLEK 128
                                  VAANHGYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDK 670
                                                                       LAHDEKSCVAASDSADIFSNDIEDYSKVPGLDSIDEVIS--SIESYPADESPRPL----
                                                                                                                                                                              PFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEPV 552
                                                                                                                                                                                                                                                                                                                                                                                                                                            -----AQCQCYPGFH-LSYDRRSCVDIDECAKNNGCEHFCENV----KGTYRCKCREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTCGSGFHF--ENLILIKKVTSCSTDNGGCEHEC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKCIYSIYEMGKRSVFI-------GCQPQCVRTIITRACWLASLAHNAKPAPGEVK 217
                                                                                                       SISVSQDTVFINNEAKVLSSDIISTNGV--IHVIDKLLSPKNLLITPKDALGRVLQNLTT 610
                                                                                                                                                                                                                     CS-NQEGGYMCSCEPGFELSEDGHSC------HDMNECLINNG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MCALGTASVWDGVNGTGTCQCGLGF----NGTAC---ETCTEGKYGIHCDQACSCVHGRC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 142; Mismatches 451;
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21.0%;
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Pred. No. 8.1e-36;
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WUH9 PRELIMINARY; PRT; 2906 AA.	SHOW
10	SUL
17 ENGALCOPISGHCS 1230	Db 12
AGYVGDGFSC	Qy 11
84 GRCECLPGWSGEHCEKSCVSGHYGAKCEETCEC 1216	Db 11
LESGRVAYPTTYASQKCGANVVGIVDYGSRANK	0у 11
LCPFGQFGRNC	Db 11
48 PDASCADLYFQDTTVGVFHLRSPLGQYKLTFDKAKEACAKEAATIATYNQLSY	Qy 10
78 GEGCRHSCQCSNGASCDRVTGFCDCPSGFMGKNCESECPEG	Db 10
15 KDNGQC	Оу 10
18 PCPDGRFGEGCNAICDCTTTNDTSMYNPFVARCDHVTGECRCPAGWTGPDCQTSCPL	Db 10
CADGVNG-GCHEHATCRMTGP	Оу 9
66 GKKGHKCDETCDSGLFGAGCKGICSCQNGATCDSVTGSCECRPGWRGKKCDR 1017	pb 9
GDGI TCTVVDFCKQK	0у 9
13 -TSNGSCECAPGWSGKKCDKACAPGTFGKDCSKKCDCADGMHCDPSDGECICPP 965	Db 9
LCETGWTAASCDTPTAVFAVCTPACSVHATCTENNTC	Оу 8
QNGAIC	Db 8
FNGTAC-	Оу 8
95 DQPCPAGYFGYDCEQKCSCADVASPHKSKVCHHVTGTCTCLPGKTGPLCDQSCAPNTYGP 854	Db 7
	Оу 8
39RCKPGYYGHHCKRMCSPGLEGAGCAMKCSCPAGIRCDPVTGDCTKKCPAGYQGNLC 794	Db 7
	Оу 8
82 PNGRCDPVFGYCTCPDGLYGQSCEKPCPHFTFGKNCRFPCKCARENSEGCDEITGKC 738	Db 6
ECCON	Qy 7
32 GVDCAHKCSCKLCDPSTGSCRCEDPEKCSDGPCPDGFYGSQCNLKCRMDC 681	Db 6
GIDCLLMNPTLGG-RCDTFTTFDIPGECGSCIFTPKCPLKS	Оу 7
83FGSTCQLSCSDCQNGGKCSMRGSGLLSKCDCPSGYTGEKCEQICRNGYW 631	Db 5
/ LNSIENEHVIRUSNALASULERGASWNILQGSELSVRCGIGSU-IGELELNEQMCREI	ζÝ

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Best Local Similarity
Matches 301; Conser
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SMART; SM00179; EGF_CA; 42.

SMART; SM00001; EGF_LIKe; 4.

PROSITE: PS00070; ALDEMYDE_DEHYDR_CYS; UNKNOWN_1.

PROSITE: PS00010; ASX_HYDROXYL; 43.

PROSITE: PS00022; EGF_1; UNKNOWN_2.

PROSITE: PS01186; EGF_2; 36.

PROSITE: PS01186; EGF_CA; 43.

Calcium-binding; EGF-Like domain; Glycoprotein; Hydroxylation; SEQUENCE 2906 AA; 313371 MW; 9EE64E727044EF58 CRC64;
   1076
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Pfam; PF00008; EGF; 46.
Pfam; PF00683; TB; 9.
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HSSP;
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InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
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QCVRTIITRACWLASLAHNAKPAPG---EVKMCALGTASVWDGVNGTGT--CQCGLGFNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGENCVGHDECTTTNMCLNGMCINEDGSFKCVCKPGFVLAPNGRCCTDVDECQTPGICMN
                                                                                                                                                                                          --CERCELD------
                                                                                                                                                                                                                                                                                                                                       DGKVCSLINVCLTN---NGGCSPFAFCNYTEQDQRICTCKP--DYTGDGIVCRGSIYGEL
: : | :| :| :| ||:|
                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCANPDYGFGEPCQPCPAKNSAEFHGLCSGGVGITVDGRDINECALDPDICANGICENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHCINNEGSFRCDC---PPGLAVGVDGRVCVDTHMRSTCYGEIKKGVCVRPFPGAVTKYE 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D--NCNG--TCHTSANCL----LDPDGKASCKCAAGF--RGNGTVCTAINACET----SN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T----ACETCTEGKYGIHCDQ-ACSCVHGRCSQGPLGDGS--CDCDVGWRGVKCDMEITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RCIPTVSSYRC-ECNMGYK-QDANGDCIDVDECTSNPCSHGDCVNTPGSYYCKCHAGFQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF135060;
P35555; 1
                                                               CAVGAAWGTECEECPKPGTKEYETLCPRGPGF---ANRGDILTGRPFYKDINECKALPGM
                                                                                               TPVTVFWPTD----
                                                                                                                                                        VIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSV----ITDSIH
                                                                                                                                                                                                                      VGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAKVL----SSDIISTNGVIH
                                                                                                                                                                                                                                                       WLNIQDNRCEVNINGATLKS----
                                                                                                                                                                                                                                                                                    PKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHV
                                                                                                                                                                                                                                                                                                                  ETETCEDVNECESNPCVNGACR-----NNLGSFHCECSPGSKLSSTGLICIGSLKGTC
                                                                                                                                                                                                                                                                                                                                                                                  RGSYRCNCNSGYEPDASGRNCIDIDECLVNRLLCD-NGLCRNT-PGSYSCTCPPGYVFRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPTKQACIDIDE------CIQNGVLCKNGRCVN---TDGSFQCICNAGF------ELTT
                                                                                                                            -CECPEGLTL---DGTGRVCLD---VRMEHCFLKWD---EDECVHPVPGKFRMDACC
                                                                                                                                                                                                                                                                                                                                                                                                              -CKAGYTGD--GIVCLEINPCLENHGGCDRNAECTQTGPNQAVCNCLPKYT--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STKADCKRTTPG-----NRVCV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD34439.1;
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                                                                                           ----KALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASD
                                                                                                                                                                                         -AACPRGFARIKGVTCEDV---NECEVFPGVCPNGRCVNNKGSFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 519.5; DB 11;
Pred. No. 4.9e-34;
Pred. Mismatches 407;
                                                                                                                                                                                                                                                       ECCATLGTA-----
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ALD DATE OF REPORT OF THE PROPERTY OF THE PROP
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Q25253
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Q25253;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                                      Davies A.G., Game A.Y., Chen Z., Williams T.J., Goodall S., McKenzle J.A., Batterham P.;
"Scalloped wings is the Lucilia cuprina Notch homologue and candidate for the modifier of fitness and asymmetry of diazi resistance.";
STRAIN-SS SEEKING;
Chen Z., McKenzie J.A., Batterham P.;
Submitted (NOV-1997) to the EMBL/GenB
EMBL; U58977; AAC36151.1; -.
                                                                                                                                                                                            STRAIN-SS
                                                                                                                                                                                                                                            [2]
SEQUENCE OF 39-265
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=SS SEEKING;
MEDLINE=96400928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Lucilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
NOTCH HOMOLOG SCALLOPED WINGS (SCL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1557
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                                                                                                           [3]
SEQUENCE OF 39-265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIC-DGGQC-TNIPGEYRCLCYDGF-MASMDMKTCIDVNECDLNPNICMFGEC-ENTKGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt NGQCLNVPGAYRCECEMGFTPASDSRSCQDIDECSFQNICVFGTCNNLPGMFHCICDDG-}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGQC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLDECANGTH-QCSINAQCVNT-PGSYRCACSEGFTGDGFTCS----DVDECAENINLCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NATGYGCYD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YGL -- DRTGGHCTDIDECADPINCVNGLCVNTPGRYE-
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                                                                                                                                                             S SEEKING;
Newsome T.,
1 (DEC-1997)
                                                                                                                                                                                       Newsome
                                                                                                                                                                                                                                                                                                  143:1321-1337(1996)
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                                                                                                             FROM
                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                             McKenzie
to the EM
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                                                                                                           N.A.
                            EMBL/GenBank/DDBJ
                                                                                                                                                                   EMBL/GenBank/DDBJ
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                                                                                                                                                                                       J.A.,
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                                                                                                                                                                                          Batterham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00023; ank; 6.

Pfam; PF00008; EGF; 36.

Pfam; PF00066; notch; 3.

PRINTS; PR00010; EGFBLOOD.

PRINTS; PR00010; EGFBLOOD.

PRINTS; PR00010; EGF_CA; 24.

SMART; SM002148; ANK; 4.

SMART; SM00001; EGF_Like; 11.

SMART; SM00001; EGF_Like; 11.

SMART; SM000088; ANK_REPEAT; 5.

PROSITE; PS00088; ANK_REP_REGION; 1.

PROSITE; PS00010; ASX_HYDROXYL; 22.

PROSITE; PS00002; EGF_1; UNKNOWN_34.

PROSITE; PS01186; EGF_2; 28.

PROSITE; PS01187; EGF_CA; 21.

ANK repeat; Calcium-binding; EGF-like do:
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InterPro;
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                                                                                                                                                  AVCNCLPKYTGDGKVCSL-INVCLT----NNGGCSPFAFCNYTEQDQRICTCKPDYTGDG
                                                                                                                                                                                                                                                            KCDMEITTDNCN--GTCHTSANCLLDPDGKASCKCAAGFRGNGTVC-TAINACETSNGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNNDTIIVRGECGKCSQQAPCPLETKPLRETRKCIYSIYFMGK--RSVFIGCQPQ----
IISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVI
                                                  QGLMSQVLRY--HVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEAKVLSSD
                                                                                 LSCEINI - NDCNSNPC
                                                                                               IVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFT-VFAPLSSSFNHEPRIKDWDQ : | : | | | | | : : : : | : :
                                                                                                                                   FKCSCALGFTGSR--CQINIDDCQSQPCRNNGICRD-SIAGYT-----CQCPPGYT--G
                                                                                                                                                                                                          DCSEDI - - DECDQGSPCEHNGVCVNTP-GSFRCNCSQGF--TGPRCETNINECESH--PC
                                                                                                                                                                                                                                                                                                ATCIDGVGSFYCRCTPGKTGLLCHLDDACTSNPCHADAICDTSPINGSYTCPCATGYKGV
                                                                                                                                                                                                                                                                                                                                                      TGENCEKDVDECAIRPSVCQNGATCTNSQGSYSCICVNGWTGPDCSENIDDCLAAACFYG
                                                                                                                                                                                                                                                                                                                                                                                                            GGTCRSTGLTYECKCPEGYQGKNCEQNIDDCPGH--LCQNGGTCI-DGINSYHCACPPNY
                                                                                                                                                                                                                                                                                                                                                                                                                                     ---CVRTIITRACWL-----ASLAHNAKPAPGEVKMCALGTASVWDGVN------
                            SNPCQYGGHCVDRVGSYMCHCLAGTS----
                                                                                                                                                                                                                                                                                                                 -----TCTEGKYGI--HCDQACS---C-VHGRCSQGPL-GDGSCDCDVGWRGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000561;
IPR000742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000800; Notch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2653 AA; 285928 MW;
                                                                                                                                                                                           LDDPGTFRCVCMPGFTGTQCEIDINEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PCKHGGTC-LNT---HGSYQCMCPAGYTGKNCESKYVPCSPSPCQN
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EGF-like.
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                                                                              -HRGKCIDGDNRFTCVCDPGFTGYLCQTQINECE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6AF2A058FEEC6329 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 -GTGTCQCGLGFNGTACE-----
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                            -GKDCEINVNE
                                                                                                                                                                                        -QSNPCL-NGGICNDMI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2653;
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development.";
Am. J. Physiol.
[2]
                                                                                                                        01-DEC-2...
FIBRILLIN-1.
Rattus norvegicus (Rat).
Rattus norvegicus (Chordata; /
                                                                                                                                                                                       Q9WUH8;
Q9WUH8;
01-NOV-1999
01-NOV-1999
01-DEC-2001
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                                                                 MEDLINE=99032689;
Kanwar Y.S., Ota F
                                                                                         SEQUENCE FROM N.A.
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                                        "Isolation of rat fibrillin-1 cDNA and
                                                     Peterson D
                                                                                                                     NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                         KCGANV
                                                                                                                                                                                                                                                                                                                                                                   CPPGTAGLICEVNENDCKRGSC----HNNGTCIDRVGGFEC
                                                                                                                                                                                                                                                                                                                                                                                            SPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYASQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSLEQLCNNGTCKEHGNI - - - - - - HRCYCKQGYTGSYCQQEINECESQPCLNGGTCRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V----NGGCHEHATCRMTGPGKHKCECKSHYVG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -QCTDYVDWCTKS--PCENGATCTQVKNQFSCRCAPGWTGK--LCDVEMVSCSDAAIRKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITCT-VVDFCKQNNGGCAKVAKCSQKGTQVSCSCKKGYKGDGYSC-IEIDPCAD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDGI-NSYNCSCLPGYTGSNCQ--YKINKCDSQPCQNGATCHENGDEYTCHCSYGYTGK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEGITGSGECLCETGWTAASCDTPTAVFAVCTPACSVHATCTENN---TCVCNLNYEGDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTACEL------CWHGRF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIDCLLMNPTLGGRCDTFTTFDIPGEC - - - GSCI - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASNPCINGGRCEDGINEFICHCPPGYGGKRCENDIDECSSNP--CQ--HGGFCVDELNAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --GVHCEINI-----NECASNPCANNGVCMDLVNGYKCECPRGFY---DPRCL-SDVDEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRS
                                                                                                                                                                                                                                                                                                                                                                                                                       IGSYACVCRKGFQGQNCE---LNIDDCSPNPCQNGGTCH-----DL----VNTFSCS
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R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                --DGVDCEPEQLPLDRC----LQDNGQCHPDASCADLYFQDTTVGVFHLR
              275:F710-F723(1998)
                                                                PubMed=9815129;
K., Yang Q., Kum
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Last sequence update)
Last annotation updat
                                                                                                                                  Craniata; Ver
Sciurognathi;
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                                        relevance
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                                                                                                                                     Muridae;
                                                                J.,
                                                                   Kashihara
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                                                                                                                                     Euteleostomi; 

; Murinae; Rat
                                       in metanephric
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Best Local :
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InterPro; IPR000561; I
InterPro; IPR001881; I
InterPro; IPR002212; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00010; ASX_HYDOXYL; 42.

PROSITE; PS00022; EGF_1; UNKNOWN_2.

PROSITE; PS01186; EGF_2; 38.

PROSITE; PS01187; EGF_CA; 41.

PROSITE; PS01187; EGF_CA; 41.

PROSITE; PS01028; ZINC_FINGER_C2H2_1; UNKNOWN_1.

Calcium-binding; EGF-11ke domain; Glycoprotein; Hydroxylation; Repeat.

Calcium-binding; EGF-11ke domain; Glycoprotein; Hydroxylation; Repeat.

SEQUENCE 2872 AA; 312069 MW; 0C4F7F3B87A80280 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR000822; Znf-C21

Pfam; PF00008; EGF; 45.

Pfam; PF00683; TB; 9.

SMART; SM00179; EGF_CA; 41.

SMART; SM00001; EGF_Like; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1999) to the EMBL; AF135059; AAD34438.1; HSSP; P35555; 1APJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Kanwar Y.S.;
                 649
                                                945
                                                                                                               893
                                                                                                                                                                                                                                                                     451
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                                                                                                                                                                                                       RIKDWDQQGLMSQVLRYHVVGCQQLLLD-NLKVTTSATTLQ------
                                                                                                                                                                                                                                                                     DYTGD--GIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEP
                                                                                                                                                                                                                                                                                                                    PNQAVCNCLPK---YTGDGKVCSLINVCLTN---NGGC--SPFAFCNYTEQDQRICTCKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GECINNQGSYTCHCRAGYQSTL--TRTECRDIDECLQNGRICNNGRCIN---TDGSFHCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WDGVNGTG--TCQCGLGFNGTACETCTEGKYGIHCDQ-ACSCVHGRCSQGPLGDGS--CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKVLPFNVTDYCQLVRYLCQNGRCIPTPGSYRCECNKGFQLDIRGECIDVDECEKNPCTG 502
                                                                           KDALGRVLQNLTTVAANHGYTKFSKLIQDSGLLSVI----TDSIHTPVTVFWPTD-----
                                                                                                                                                                                                                                                                                                  PGSFVCTC-PKGFVYKPDLKTCEDIDECESSPCINGVCKNSPGSF---
                                                                                                                                                                                                                                                                                                                                                                  CALDPDICPNGICENLRGTYKCICNSGYEVDITGKNCVDINECVLNSLLCD-NGQCRNT-
                                                                                                                                                                                                                                                                                                                                                                                    -----CVCKAGYTGD--GIVCLEINPCLENHGGCDRNAECTQTG
                                                                                                                                                                                                                                                                                                                                                                                                                             RGQCVKPLFGAVTKSECCCASTEYAFGEACQPCPAQNSAEYQALCSSGPGMTSAGSDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGTVCTAINACET ---- SNGGC ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNAGFHVTRDGKNCE---DMDECSIRNMCLNGMC----INEDGSFKCICKPGFQLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDVGWR----GVKCDMEITTDNC-----NGTCHTSANCLLDPDGKASCKCAAGFR--G
                                                                                                                                                                                                                                       ESTLDPTKTICIETIKGT - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGRYCKDINECETPGICMNGRCVNTDGSYRCECFPGLAVGLDGRVCVDTHMRSTCYGGYR
                                             -DATGRICLDIRL-----ETCFLKYDDEECTLPIAGRHRMDACCSSVGAAWGTEECEEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                KALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALASDLPRSASWKTLQGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                         -SVSQDTVFINNEAKVLSSDIISTNGVI---HVIDKLLSPKNLLITP
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EGF-like.
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                                                                                                                                                                        -CWQTVIDGRCEININGATLKSECCSSLGAAWGSPCTICQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 499.5; DB 11;
Pred. No. 2.4e-32;
Pred. No. 2.2e-32;
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                       MGD; MGI:97364; Notch2.
InterPro; IPR002110; ANK.
InterPro; IPR000152; Asx_hydroxy1.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
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01-JAN-1998
01-JAN-1998
01-DEC-2001
                                                                                                                                                                                                    single copy of mouse Notch2 gene.";
Submitted (JUI-1994) to the EMBL/GenBank/DDBJ
EMBL; D32210; BAA22094.1; -
HSSP; P16109; 1FSB.
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                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57B/6; TISSUE-THYMUS;
Hamada Y., Higuchi M., Tsujimoto Y.;
"Complete amino acid sequence and mutliform transcripts
                                                                                                                                                                                                                                                                                                                                                                                                                                Lardelli M., Lendahl U.;
"Motch A and Motch B - two mouse
wide variety of tissues.";
Exp. Cell Res. 204:364-372(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57B/6; TISSUE=THYMUS;
MEDLINE=3178563; PubMed=8440332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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EGF_Ca.
EGF_II.
Notch.
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Best Local S
Matches 282
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SMART; SM000179; EGF_CA; 22.

SMART; SM00001; EGF_Like; 12.

SMART; SM00004; NL; 3.

SMART; SM00004; NL; 3.

PROSITE; PS50008; ANK_REPEAT; 4.

PROSITE; PS50010; ASX_HYDROXYL; 22.

PROSITE; PS00010; ASX_HYDROXYL; 22.

PROSITE; PS00010; AGF_1; UKKNOWN_33.

PROSITE; PS01187; EGF_1; UKKNOWN_33.

PROSITE; PS01187; EGF_CA; 22.
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Pfam; PF00008; EGF; 35.
Pfam; PF000066; notich; 2.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR01452; NOTCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydroxylation; SEQUENCE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANK repeat; Calcium-binding; EGF-like Hydroxylation; Repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQPNACQNGGTCTNRNGGYGCVCVNGWSGDDCSENID-------DCAYA-----
                          PYTGKNCQTVLAPCSPNPCENAAVCKEAPNFESFSCLCAPGWQGKRCTVDVDECISKPCM
                                                       PTLGGRCDTFTTFDIPGECG
                                                                                                            SDLPRSASWKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGVAYGIDCLLMN
                                                                                                                                         GWVGVNCE-
                                                                                                                                                                  GLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKLKSYLKFHVIRDSKALA
                                                                                                                                                                                               RKGATCINDVNGFRCICPEGPHHPSCYSQVNECLSNPCIHGNCTGGLSGY - - -
                                                                                                                                                                                                                   KVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTVAANHGYTKFSKLIQDS
                                                                                                                                                                                                                                                                                                          M--GAICSDQI-DECYSSPC-----LNDGRCIDLVN-GYQCNCQPGTSGLNCEINFDD
                                                                                                                                                                                                                                                                                                                                     TGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGPGPFTVFAPLSSSFNHEPRIKD
                                                                                                                                                                                                                                                                                                                                                                   -HPNGYECQCATGFTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GWRGVKCDMEITTDNCNG-TCHTSANCLLDPDGKASCKCAAGFRGNGTVC-TAINACET-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNGQYICTCPQGYKGADCTEDVD----ECAMANSNPCEHAGKCVN---TDGAFHCECLK
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 -KGV-
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                                                                                                                                       -----VDKNECLSNPCQNGGTCN----NLVNGY-
                                                                                                                                                                                                                                                                               -RYHVVGCQQLLLDNLKVTTSATTLQGEPVSISVSQDTVFINNEA
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22.7%;
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Pred. No. 1.5e-31;
9; Mismatches 445;
                                                                                                                                                                                                                                                                                                                                                                   ILCDENIDNCDPDP-CHHGQCQDGIDSYTCICNPGY
                                                                                 NIDECASNP - - C - - LNQGTCFDDVSGYTCHCML - -
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KKKCIYNPLPFRRNVEGCQN--LCTVVIQTPR
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                                                       SCIFTP---
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                                                    --KCPLK--
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OSCRAS;

OGGAS;

O 1 MAR-2001 (TrEMBLrel. 16,
JT 01-MAR-2001 (TrEMBLrel. 16,
DT 01-DEC-2001 (TREMBLREL. 19)

OT 01-DEC-2001 (TREMBLREL. 19)
                                                                InterPro; IPR002110; ANK.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
InterPro; IPR0001881; EGF_Ca.
InterPro; IPR0001438; EGF_II.
InterPro; IPR0002049; Laminin_EGF.
InterPro; IPR000800; Notch.
                                                                                                                                                                              Holland L.Z., Burgtorf C., Holland N.D., Lehrach H., Tan Abi-Rached L., Pontarotti P., Lardelli M.;
"Cloning and developmental expression of the amphioxus on the Notch (AmphiNotch): evolutionary conservation of multip domains in amphioxus and vertebrates.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases EMBL; Y12539; CAC19873.1;
HSSP: P00740; IEDM.
          PRINTS;
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Enkaryota; Metazoa;
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                                       Pfam; PF00008; EGF; 36. Pfam; PF00066; notch; 3
                                                                                                                                                                                                                                                                                                  TISSUE=LARVA;
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                             Branchiostoma
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          PR00010;
PR00011;
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tazoa; Chordata;
         EGFBLOOD.
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. 16, Last sequence upo
. 19, Last annotation u
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Best Local S
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SMART; SM00111; EGF; 37.
SMART; SM001179; EGF_CA; 34.
SMART; SM00001; EGF_11ke;
SMART; SM00004; NL; 3.
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Local Similarity 22.1%; Pr
hes 271; Conservative 107;
                                                                                                                                                                                                                                                                                                   GYEGNNCEREIDECASSPCHNGGI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CENNINECAN-GPCRNGAHCS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNICLNCGTCHNTYGGYSCVCVNGWIGDDCSENF - - DDCASAACFDGATC - HDRVGFFMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P------LGDGSCDCDVGWRGVKCDMEITTDNC-NGTCHTSANCLLDPDGKASC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHCMSGFTGDDCEVNVDDCVDHLCENGAACVDGVNEYTCTCPSQWAGRYCNEDVDECMQS
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YT----CSCMPGFGGTNCEEDIDECYSNPCQNGGQCIDAVNGYACDCVVGFIGTNCQTNK
                             YTPMGQCLCHTGFNGTACEL----
                                                                                       NVEGCONLCTVVIQTPRCCHGYFMPDC-----
                                                                                                                     TELAPCRPNPCENLGACIPSADYQTFTCNC:
                                                                                                                                                    TFTTFDIPGEC --
                                                                                                                                                                               CQCLPGYE-GVNCDINTD--ECASNP--CQ--NGGRCLDGVNNYVCDCDL--PFVGTNCQ
                                                                                                                                                                                                           WKTLQGSELSVRCGTGSDIGELFLNEQMCRFIHRGLLFDVGVAYGIDCLLMNPTLGGRCD
                                                                                                                                                                                                                                        VNECESSPCAHGTCQDGINDYTCTCENGYEGKNCDVNIDECASNPCQHEGQCDDGIGRYE
                                                                                                                                                                                                                                                                       DN---
                                                                                                                                                                                                                                                                                                                                                           SDPCQNGGTCEDLVNGYRCNCLAGTSGSNCEVNQDDCTGNLCVHGVCQDGLNDYTCQCDG
                                                                                                                                                                                                                                                                                                                                                                                                                    TYACTCLEGFTGTDCEINIDDCQSNQCQHGTCVDGVASFTCSCEPGYNGPLCESPVDECD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYTEQDORICTCKPDYTGDGIVCRGSIYGELPKNP-----STSQYFFQLQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECAPG - - KTGLLCHLDDACESS - - PCNEGAICD - TNPVNGQPICTCPDGY - - EGQLCMQD
                                                             NGAPCVNL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -EHAVRELAGPGPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - IDDIGEFRCACMPGFAGD--LCETDV-DECASSPCLNGLCRDGINKYECECDPGFEGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INPCLENHGGCDRNAECTQTGPNQAVCNCLPKYTGDGKVCSL-INVCLTNNGGCSPFAFC
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PS50297; ANK_REP_REGION; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASX_HYDROXYL; 1.
                                                                                                                                                  -GSCI----FTPKCPLKSKPKGVK-----KKCIYNPLPFRR
                                                                                                                                                                                                                                                                      KDKLKSY-LKFHVIRDSKALASDLPRSAS-----
                                                                                                                                                                                                                                                                                                                               FSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -EPVSISVSQDTVFINNEAKVLSSDIISTNGVI--HVIDKL-
                                                            -EGDFRCDCLMGFAGELCSVNIDDCDPDPCHNGGTCNDGINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 486.5; DB 5
Pred. No. 2.5e-31;
                                                                                                                                                                                                                                                                                                                                                                                        -LSPKNLLITPKDALGRVL---
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                                                                                                                     ----ADGFEGETCADDINECQSNPC---K
                                                                                                                                                                                                                                                                                                   -CHDLVNAF----SCECPPGYHDQLCYSN
                                                                                       -QACPGGPD----TPCNNRGMCRD---L
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                              ·CWHGRFGPDCQPR-
                                                                                                                                                                                                                                                                                                                                                                                        -- QNLTTVAANH
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X MEDLINE-94150718; pubMed-7906398;

X MEDLINE-94150718; pubMed-7906398;

X MEDLINE-94150718; pubMed-7906398;

X MISON R., Ainscough R., Anderson K., Baynes C., Berks M.,

X Milson R., Ainscough R., Anderson K., Copsey T., Cooper J., Coulson A.,

X Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

X Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

X Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

X Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

X Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

X Jones M., Kershaw J., Kirsten J., Mortimore B., O'Callaghan M.,

X A Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,

X A Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

X A Smaldon N., Smith A., Sonnhammer E., Stadden R., Sulston J.,

X A Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

**T elegans.";

**T elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19, Y47H9C.4 PROTEIN (CED-1). Y47H9C.4 OR CED-1.
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            Cell 104:43-56(2001).
EMBL; AL032657; CAA21739.1;
EMBL; AF332568; AAG60061.1;
InterPro; IPR000561; EGF-11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans
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                                                                                    "CED-1 is a Transmembrane R
Engulfment in C. elegans.";
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NCBI_TaxID=6239;
                                                                                                                                       MEDLINE=21097720;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harris
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                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                            368:32-38(1994).
                                                                                                                   21097720; PubMed=11163239; Hartwieg E., Horvitz H.R.;
IPR002174;
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                EGF-like
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                                                                                                      Receptor
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Last annotation updat
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                                                                                                        Cell Corpse
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Best Local Similarity 22.2
Matches 251; Conservative
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SMART; SM00001; EGF_l1ke; 5.
SMART; SM00261; FU; 2.
PROSITE; PS00022; EGF_1; UNKNOWN_15.
PROSITE; PS01186; EGF_2; 11.
EGF-11ke domain; Glycoprotein.
EGF-11ke domain; Glycoprotein.
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 834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VH-GRCSQGPLGDGSCDCDVGWR------GVKCDMEITTDNCNGTCHTSANCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCSVGTWGLGCSKSCDCENGANCDPELGTCICTSGFQGERCEKPCPDNKWGPNCVKSCPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HVCTVKTIVDDYELKKVIHTVVYNDTEQCLNPLTGFQCTVEKRGQ--KASYQRQL---VK
                                                                                                               LLFDVGV---AYGIDCLLMNPTLGGRCDTFTTFDIPGECGSC---IFTPKCPLK-SKPKG
                                                                                                                                                                                                                                                                                                                                                     CPLDFYGP---NCAHQCQC---NQRG-----VGCD------
                                                                                                                                                                                                                                                                                                                                                                                 GPFTVFAPLSSSFNHEPRIKDWDQQGLMSQVLRYHVVGCQQLLLDNLKVTTSATTLQGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNGGKCNK----EGKCVCSDGWGGEFCLNKCEEGKFGAECKFE-----CN--CQNGATC- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGADCSKTCTCVRENTLMCAPNTGFCRCKPGFYGDN--CEL--ACSKDSYGPNCEKQAMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGG-CDRNAECTQ----TGPNQAVCNCLPKYTGDGKVCSLINVCLTNNGG--CSPFAFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --GCST---KADCKR--TTPG------NRVCVCKAGYTGDGIVCLEINPCLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNTNGKCICKSGYHGALCENECSVGFFGSGCTQKCDCLNNQNCDSSSGECKCIGWTGKHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDPDGKASCK-------CAAGFRGNGTV--CTAIN--ACETSNG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEKYVKQCCDGYYQTKDHFCLPDCNPPCKKGKCIEPGKC-----ECDPGYGG-KYCAS
 PC--NNRG-MCRDLYTPM-----
                                                           VKKKCIYNPLPFRRNVEGCQNLC----TVVIQTPRCCHGYFMPDCQACPGGP-----DT
                                                                                                                                                                                       KSYLKFHVIRDSKALASDLPRSASWKTLQGSELSVRCGTGSDIG-ELFLNEQMCRFIHRG
                                                                                                                                                                                                                                                      AANHGYTKFSKLIQDSGLLSVITDSIHTPVTVFWPTDKALEALPPEQQDFLFNQDNKDKL
                                                                                                                                                                                                                                                                                                                   VSISVSQDTVFINNEAKVLSSDIISTNGVIHVIDKLLSPKNLLITPKDALGRVLQNLTTV
                                                                                                                                                                                                                                                                                                                                                                                                                    DWNHASECNPETGSCVCKPGRTG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NYTEQDQ-----RICTCKPDYTGDGIVCRGSIYGELPKNPSTSQYFFQLQEHAVRELAGP 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIGCSRGRFGLQCKQNCTCPGLEFSDSNASCDAKTGQCQCESGYKGP--KCDERKCDAEQ
                             -----YG-----ESCELSCPCSDASCSKQTGKC------LCPLGTKGVSCDQ
                                                                                           ANCDIGCPEGSYGPGCKLHCKCVNGKCDKET----GEC-TCQPGFFGSDCSTTCSKGK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----LGTASVWDGVNGT------GTCQCGLGFNGTACE-TCTEGKYG1HCDQACSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.1%;
22.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 480.5; DB 5;
; Pred. No. 2.2e-31;
98; Mismatches 341;
                                                                                                                                                                                                                         -HCPADTF-----
-GQCL-CHTGFNGTACE-LCWHGRFGPDCQP-RS
                                                                                                                                                         -GANCEKRCKCPKGIGCDPITGECTCPAGLQG
                                                                                                                                                                                                                                                                                                                                                                                                                  ----KNCSE--
                                                                                                                                                                                                                                                                                     -GADGKCOCDRGWTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
 878
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                                                                                                                                                                                                                                                                                                                     611
                                                                                                                                                                                                                                                                                                                                                                                   551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163
                                                                                                                                                         541
                                                                                                                                                                                          730
                                                                                                                                                                                                                                                                                                                                                                                                                  460
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Qy
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                                                                                                                                                                                                                                                                                                                                                                                    DЬ
B
                                          QУ
                                                                                         Вb
                                                                                                                                                                                                                                                                                      В
                                          1030 EPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHL-RSPLGQYKLTFD
                                                                                                                                                                                                                                                                                                                                                                                    631
                                                                                                                       IEIDPCADGVNG-GCHEHATCRWTGPG-----KHKCECKSHYVGD-------GVDC 1029
                                                                                                                                                                                                                                                                                                                                                                                    KCDPNTFGFLCQETVTPSPCASTDPKNGVCLSCPPGSSGIHCEHNCPAGSYGDGCQQVCS
                                                                                                                                                                                       CICPAGLE -- GALCTRPCSAGFWGNGCRQVCRCTSEYKQCNAQTGECSCPAGFQGD -- RC
                                                                                                                                                                                                                                       CVCNLNYEGDGITCTVVDFCKQNNGGCAKVAKCSQKGTQVS-----CSCKKGYKGDGYSC 986
                                                                                                                                                                                                                                                                                      {\tt CADGHGCD---PTTGECICEPGYHGKTCSEKCPDGKYGYGCALDCPKCASGSTCDHINGL}
                                                                                           {\tt DK--PCEDGYYGPDCIKKCKCQGTATSSCNRVSGACHCHPGFTGEFCHALCPESTFGLKC}
                                                                                                                                                                                                                                                                                                                                     CSEHGQCDEGITGSGECLCETGWTAASCD--TPTAVF----AVCTPACSVHATCTE-NNT
-C-PKDGCGDGYECDAAIGCCHVDQMSCGKAKQEFE
                                                                                                                                                                                            803
                                                                                                                                                                                                                                                                                      747
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Search completed: June 17, 2002, 12:35:05 Job time: 321 sec

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